



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 151497

TO: Sumesh Kaushal  
Location: REM-2B85/2C70  
Art Unit: 1636  
Wednesday, April 27, 2005

Case Serial Number: 10/735014

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen 1a69  
Phone: 571-272-2518

barbara.obryen@uspto.gov

### Search Notes

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2005, 19:00:41 ; Search time 122 Seconds  
(without alignments)

1366.342 Million cell updates/sec

Title: US-10-735-014-83

Perfect score: 2211

Sequence: 1 MFFGEGSLTYTLVIICFLT.....LARKYSLDYLVINGIYVDI 431

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	431	2 AAY17834	Aay17834 Human PRO
2	2211	100.0	431	3 AAB33428	Aab33428 Human PRO
3	2211	100.0	431	3 AAB01325	Aab01325 Human PRO
4	2211	100.0	431	3 AAB34739	Aab34739 Human sec
5	2211	100.0	431	4 AAB95464	Aab95464 Human PRO
6	2211	100.0	431	4 AAB65299	Aab65299 Human PRO
7	2211	100.0	431	6 ABUS5934	Abu5934 Human sec
8	2211	100.0	431	6 ABUS58114	Abu58114 Human PRO
9	2211	100.0	431	6 ABUS59192	Abu59192 Novel hum
10	2211	100.0	431	6 ABUS2704	Abu2704 Human sec
11	2211	100.0	431	6 ABUS60623	Abu60623 Human sec
12	2211	100.0	431	6 ABUS14005	Abu14005 Human PRO
13	2211	100.0	431	6 ABUS60244	Abu60244 Human PRO
14	2211	100.0	431	6 ABUS72590	Abu72590 Novel hum
15	2211	100.0	431	6 ABUS64930	Abu64930 Human sec
16	2211	100.0	431	6 ABUS8364	Abu8364 Novel hum
17	2211	100.0	431	6 ABUS7250	Abu7250 Human PRO
18	2211	100.0	431	6 ABUS59339	Abu59339 Human sec
19	2211	100.0	431	6 ABO26036	Abo26036 Human PRO
20	2211	100.0	431	6 ABUS56315	Abu56315 Human sec
21	2211	100.0	431	6 ABUS60355	Abu60355 Novel hum
22	2211	100.0	431	6 ABUS9045	Abu9045 Human sec
23	2211	100.0	431	6 ABUS92423	Abu92423 Novel hum
24	2211	100.0	431	6 ABUS59488	Abu59488 Novel hum
25	2211	100.0	431	6 ABUS92254	Abu92254 Novel hum

#### ALIGNMENTS

##### RESULT 1

AAY17834

ID AAY17834 standard; protein; 431 AA.

XX AC AAY17834;

XX DT 12-AUG-1999 (first entry)

XX DE Human PRO361 protein sequence.

XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;

XX PW secreted protein; transmembrane protein; inflammation disorder.

XX OS Homo sapiens.

XX PN WO9928462-A2.

XX PD 10-JUN-1999.

XX PF 01-DEC-1998; 98WO-US025108.

XX PR 03-DEC-1997; 97US-0067411P.

XX PR 11-DEC-1997; 97US-0069278P.

XX PR 11-DEC-1997; 97US-0069334P.

XX PR 12-DEC-1997; 97US-0069335P.

XX PR 16-DEC-1997; 97US-0069425P.

XX PR 16-DEC-1997; 97US-0069694P.

XX PR 16-DEC-1997; 97US-0069696P.

XX PR 16-DEC-1997; 97US-0069702P.

XX PR 17-DEC-1997; 97US-0069870P.

XX PR 17-DEC-1997; 97US-0069873P.

XX PR 18-DEC-1997; 97US-0068017P.

XX PR 05-JAN-1998; 98US-0070400P.

XX PR 09-FEB-1998; 98US-0074086P.

XX PR 09-FEB-1998; 98US-0074092P.

XX PR 25-FEB-1998; 98US-0075945P.

XX (GETH ) GENENTECH INC.

XX PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;

XX WPI; 1999-371118/31.

XX DR N-PSDB; AAX80059.

XX PT Nucleic acids encoding PRO secreted and transmembrane proteins.

XX PS Claim 12; Fig 37; 123pp; English.

XX

26	2211	100.0	431	6 ABU10960	Abu10960 Human PRO
27	2211	100.0	431	6 ABU11316	Abu11316 Human PRO
28	2211	100.0	431	6 ABU67135	Abu67135 Human PRO
29	2211	100.0	431	6 ABU81712	Abu81712 Novel hum
30	2211	100.0	431	6 ABU86651	Abu86651 Human sec
31	2211	100.0	431	6 ABO34165	Abo34165 Human PRO
32	2211	100.0	431	6 ADA38026	Ada38026 Human sec
33	2211	100.0	431	6 ADA21712	Ada21712 Human sec
34	2211	100.0	431	6 ADA10499	Ada10499 Human sec
35	2211	100.0	431	6 ADA18043	Ada18043 Human PRO
36	2211	100.0	431	6 ADA28151	Ada28151 Human sec
37	2211	100.0	431	6 ADA94731	Ada94731 Human sec
38	2211	100.0	431	6 ADA38956	Ada38956 Human sec
39	2211	100.0	431	6 ADA93077	Ada93077 Human sec
40	2211	100.0	431	7 ABO53251	Abo53251 Human sec
41	2211	100.0	431	7 ADA22638	Ada22638 Human sec
42	2211	100.0	431	7 ABO22621	Abo22621 Human sec
43	2211	100.0	431	7 ADA06804	Ada06804 Human sec
44	2211	100.0	431	7 ADA39497	Ada39497 Human sec
45	2211	100.0	431	7 ADB96523	Adb96523 Human PRO

CC The present invention describes nucleic acids encoding PRO secreted and  
CC transmembrane proteins used therapeutically. The PRO proteins have  
CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive  
CC activity. The proteins and polynucleotides can be used in therapy.  
CC identification of homologues, raising antibodies and design of probes and  
CC primers. They can be used in a range of diseases related to proteins that  
CC they have homology with, e.g. a PRO protein having homology to complement  
CC proteins may be used in inflammatory responses

XX Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 2; Length 431;  
Best Local Similarity 100.0%; Pred. No. 4,9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGEGSLTVLIIICFLTRLASQNLKSLKSLDVEDVVIQSLSGIRGNEPVTSTQ 60  
DB 1 MFPGEGSLTVLIIICFLTRLASQNLKSLKSLDVEDVVIQSLSGIRGNEPVTSTQ 60  
QY 61 EDCINSCCSTKNIISGDKACNLMIIDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
DB 61 EDCINSCCSTKNIISGDKACNLMIIDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
QY 121 TDFSLTRLNLSQELPQEDSLHGFQSOAVTFLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
DB 121 TDFSLTRLNLSQELPQEDSLHGFQSOAVTFLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
QY 181 HLEKLFKMDASAQLLAYKEKGHSQSSQSFSDQEIHLHPENVGALPATVAVASPHTTSA 240  
DB 181 HLEKLFKMDASAQLLAYKEKGHSQSSQSFSDQEIHLHPENVGALPATVAVASPHTTSA 240  
QY 241 TPKPATLLPTNASVTPSGTSQPOLATTPVTTVTSQPPPTLIISTVTFRAATLQAWATT 300  
DB 241 TPKPATLLPTNASVTPSGTSQPOLATTPVTTVTSQPPPTLIISTVTFRAATLQAWATT 300  
QY 301 AVLTTFQAPDTSKGSLETIPTEISNLNTGNVYNPTALSMNVESSTMNKTASWEGR 360  
DB 301 AVLTTFQAPDTSKGSLETIPTEISNLNTGNVYNPTALSMNVESSTMNKTASWEGR 360  
QY 361 EASPGSSSGSVENQYGLPEKWLIIIGSLFGVLVIGLVLLGRILSELRRKRSRL 420  
DB 361 EASPGSSSGSVENQYGLPEKWLIIIGSLFGVLVIGLVLLGRILSELRRKRSRL 420  
QY 421 DYLLINGIYVDI 431  
DB 421 DYLLINGIYVDI 431

RESULT 2  
AAB33428  
ID AAB33428 standard; protein; 431 AA.

XX AAB33428;

XX 29-JAN-2001 (first entry)

DE Human PRO361 protein UNQ316 SEQ ID NO:72.

XX Human; immune related disease; diagnosis; anti-inflammatory; cardiant;  
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;  
XX haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
XX antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
XX osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
XX autoimmune thrombocytopaenia; immune-mediated renal disease;  
XX demyelinating disease; hepatobiliary disease; Whipple's disease;  
XX inflammatory bowel disease; gluten-sensitive enteropathy;  
XX autoimmune disease; immune-mediated skin disease; allergic disease;  
XX immunological disease; transplantation associated disease;  
XX graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX WO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99US-0123618P.

XX 12-MAR-1999; 99US-0123957P.

XX 12-MAR-1999; 99US-0125775P.

XX 12-APR-1999; 99US-0128849P.

XX 20-APR-1999; 99WO-US008615.

XX 28-APR-1999; 99US-0131445P.

XX 04-MAY-1999; 99US-0132371P.

XX 14-MAY-1999; 99US-0134287P.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0148222P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 03-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 22-FEB-2000; 2000WO-US004414.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53.

N-PSDB; AAC58593.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 30; 309pp; English.

The present invention describes sixty four human PRO proteins which can  
be used in the treatment of immune related diseases. The human PRO  
proteins, anti-PRO antibodies, agonists and antagonists are useful for  
treating and diagnosing immune related disorders. The disorders are  
selected from systemic lupus erythematosus, rheumatoid arthritis,  
osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central and



CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
 CC or immune-mediated skin diseases, allergic diseases, immunological  
 CC diseases of the lung, and transplantation associated diseases including  
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578  
 CC represent PCR primers and hybridisation probes used in the isolation of  
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
 CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 3; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGGSGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVWDIOSSLSKGRGNEPVYTSQ 60  
 DB 1 MFPGGSGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVWDIOSSLSKGRGNEPVYTSQ 60  
 QY 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
 DB 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
 QY 121 TDFPSLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
 DB 121 TDFPSLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
 QY 181 HLEKLFKMEASQAQLLAYKEKGHSQSSQFSSDOEIAHLHPENVSAIPATVAVASPHTTSA 240  
 DB 181 HLEKLFKMEASQAQLLAYKEKGHSQSSQFSSDOEIAHLHPENVSAIPATVAVASPHTTSA 240  
 QY 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT 300  
 DB 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPPTTLISTVFTRAAATLQAMATT 300  
 QY 301 AVLTTTFQAPTDKSGLETIPFTEISNLTLNTGNVNPALSNVSVESMTAKTASWEGR 360  
 DB 301 AVLTTTFQAPTDKSGLETIPFTEISNLTLNTGNVNPALSNVSVESMTAKTASWEGR 360  
 QY 361 EASPGSSSGSPENQYGLPFKKWLLIGSLFGVLFLVGLVGLILSESRLRRKYSRL 420  
 DB 361 EASPGSSSGSPENQYGLPFKKWLLIGSLFGVLFLVGLVGLILSESRLRRKYSRL 420  
 QY 421 DYLINGIYVDI 431  
 DB 421 DYLINGIYVDI 431

RESULT 3  
 AAB01325  
 ID AAB01325 standard; protein; 431 AA.

AC AAB01325;

XX 25-SEP-2000 (first entry)

DT Human PRO361 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;  
 KW PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353;  
 KW PRO361; PRO365; transmembrane polypeptide; antibody; screening;  
 KW detection; inhibition; probe; primer; human.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..25  
 FT /label= Signal peptide

FT Modified-site 4..10

FT /note= "N-myristoylation site"

FT Modified-site 48..54

FT /note= "N-myristoylation site"

FT Modified-site 50..57  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT Modified-site 72..76  
 FT /note= "N-glycosylation site"  
 FT Modified-site 222..226  
 FT /note= "N-glycosylation site"  
 FT Modified-site 251..255  
 FT /note= "N-glycosylation site"  
 FT Modified-site 315..321  
 FT /note= "N-myristoylation site"  
 FT Modified-site 327..331  
 FT /note= "N-glycosylation site"  
 FT Modified-site 352..356  
 FT /note= "N-glycosylation site"  
 FT Domain 384..405  
 FT /label= Transmembrane domain  
 FT Modified-site 415..419  
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT W0200032776-A2.

PN 08-JUN-2000.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1998; 98WO-US025108.

PR 16-DEC-1998; 98US-0112850P.

PR 22-DEC-1998; 98US-0113296P.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

PI Hillan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;

XX WPI; 2000-412324/35.

DR N-PSDB; AAA49567.

XX New human nucleic acids encoding secreted and transmembrane polypeptides,

PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic

PT agents.

XX Claim 12; Fig 32; 187pp; English.

XX New human nucleic acids encoding secreted and transmembrane polypeptides

CC which are designated as PRO polypeptides are described The membrane-bound

CC proteins have various industrial applications, including as

CC pharmaceutical and diagnostic agents. The membrane-bound proteins can

CC also be employed for screening of potential peptide or small molecule

CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO

CC antibodies are useful for the affinity purification of PRO from

CC recombinant cell culture or natural sources

XX Sequence 431 AA;

SQ Query Match 100.0%; Score 2211; DB 3; Length 431;

Best Local Similarity 100.0%; Pred. No. 4.9e-173;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPGGSGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVWDIOSSLSKGRGNEPVYTSQ 60

DB 1 MFPGGSGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVWDIOSSLSKGRGNEPVYTSQ 60

QY 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120

DB 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120

QY 121 TDFPSLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

DB 121 TDFPSLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

QY 181 HLEKLFKMEASQAQLLAYKEKGHSQSSQFSSDOEIAHLHPENVSAIPATVAVASPHTTSA 240

Db 181 HLEKLFKMDASAOQLLAYKEGHQSQSFSDQEIHLHPENVSALPATVAVASPHTTSA 240  
Qy 241 TPKEATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLISTVTRAAATLOAMATT 300  
Db 241 TPKEATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLISTVTRAAATLOAMATT 300  
Qy 301 AVLTTFQAPDSDSGSLTETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
Db 301 AVLTTFQAPDSDSGSLTETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
Qy 361 EASPGSSSQSVNPNQYGLPEKFKWLLIGSLFGVLFLVIGLVLLGRILSRLKRYSRRL 420  
Db 361 EASPGSSSQSVNPNQYGLPEKFKWLLIGSLFGVLFLVIGLVLLGRILSRLKRYSRRL 420  
Qy 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431  
RESULT 4  
ID AAB34739 standard; protein; 431 AA.  
XX AC AAB34739;  
XX DT 26-JAN-2001 (first entry)  
XX DE Human secreted protein encoded by DNA clone vo27 1.  
XX KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;  
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;  
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;  
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;  
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;  
KW psoriasis.  
XX OS Homo sapiens.  
XX FN WO200055375-A1.  
XX PD 21-SEP-2000.  
XX PF 17-MAR-2000; 2000WO-US007285.  
XX PR 17-MAR-1999; 99US-0124808P.  
XX PR 17-MAR-1999; 99US-0124916P.  
XX PR 17-AUG-1999; 99US-0149639P.  
XX PR 01-OCT-1999; 99US-0157247P.  
XX PR 29-NOV-1999; 99US-0167824P.  
XX PR 15-FEB-2000; 2000US-0182711P.  
XX PA (ALPHA-) ALPHAGENE INC.  
XX PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
XX WPI; 2000-638211/61.  
XX DR N-PSDB; AAC59840.  
XX PT Novel proteins and polypeptides useful for the treatment of e.g multiple  
PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,  
PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.  
XX PS Claim 114; Page 453-455; 493pp; English.  
XX CC This invention relates to 59 human secreted proteins and the nucleotide  
CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745  
CC represent the proteins and their encoding nucleotide sequences, and  
CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for  
CC the DNA sequences are represented by sequences AAC59847-C59596. The  
CC proteins exhibit neuroprotective, dermatological, immunosuppressive,  
CC antiinflammatory, antianemic, nootropic, antiparkinsonian,  
CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,

CC antibacterial, virucide, and fungicide activity. The proteins and  
CC nucleotide sequences are useful as nutritional sources or supplements and  
CC in research. The proteins are useful for treating immune deficiency and  
CC disorders, which may be genetic or resulting from infections, autoimmune  
CC disorders such as multiple sclerosis, systemic lupus erythematosus,  
CC rheumatoid arthritis, and for treating myeloid or lymphoid cell  
CC deficiencies such as anaemias by regulating haematopoiesis. The proteins  
CC are also useful in compositions for bone, cartilage, tendon, ligament  
CC and/or nerve tissue growth or regeneration, for wound healing, tissue  
CC repair and replacement and in the treatment of central and peripheral  
CC ulcers. Other uses include in the treatment of wounds and Parkinson's  
CC nervous system and neuropathies such as Alzheimer's and Parkinson's  
CC diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,  
CC such as spinal cord disorders, head trauma and stroke. The proteins may  
CC also be used as a contraceptive, and for treating coagulation disorders  
CC such as haemophilias. The protein and nucleotide sequences with cadherin  
CC activity are useful for treating cancer. Other uses for the protein  
CC include for inhibiting the growth, infection or function of, or killing,  
CC infectious agents such as bacteria, virus, fungi and other parasites, for  
CC effecting bodily characteristics such as height, weight, hair colour,  
CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,  
CC catabolism, anabolism, processing, utilization, storage or elimination of  
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,  
CC effecting behavioural characteristics, providing analgesic effects and  
CC for treating hyperproliferative disorders such as psoriasis  
XX XX Sequence 431 AA;  
Query Match 100.0%; Score 2211; DB 3; Length 431;  
Best Local Similarity 100.0%; Pred. NO. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFEGGEGSLYTVIICFLTRLRSASQCLKSLKSLDVEDVVIDIQSSLKIGRNEPVYSTQ 60  
Db 1 MFEGGEGSLYTVIICFLTRLRSASQCLKSLKSLDVEDVVIDIQSSLKIGRNEPVYSTQ 60  
Qy 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCFNEEACPLKPAKGLMSYRII 120  
Db 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCFNEEACPLKPAKGLMSYRII 120  
Qy 121 TDFPPLTRNLPSOELPOEDSLHGHQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
Db 121 TDFPPLTRNLPSOELPOEDSLHGHQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
Qy 181 HLEKLFKMDASAOQLLAYKEGHQSQSFSDQEIHLHPENVSALPATVAVASPHTTSA 240  
Db 181 HLEKLFKMDASAOQLLAYKEGHQSQSFSDQEIHLHPENVSALPATVAVASPHTTSA 240  
Qy 241 TPKEATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLISTVTRAAATLOAMATT 300  
Db 241 TPKEATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLISTVTRAAATLOAMATT 300  
Qy 301 AVLTTFQAPDSDSGSLTETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
Db 301 AVLTTFQAPDSDSGSLTETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
Qy 361 EASPGSSSQSVNPNQYGLPEKFKWLLIGSLFGVLFLVIGLVLLGRILSRLKRYSRRL 420  
Db 361 EASPGSSSQSVNPNQYGLPEKFKWLLIGSLFGVLFLVIGLVLLGRILSRLKRYSRRL 420  
Qy 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431  
RESULT 5  
ID AAB95464 standard; protein; 431 AA.  
XX AC AAB95464;  
XX DT 26-JUN-2001 (first entry)  
XX XX

DE Human protein sequence SEQ ID NO:17950.  
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX Homo sapiens.  
 XX EP1074617-A2.  
 XX 07-FEB-2001.  
 XX 28-JUL-2000; 2000EP-00116126.  
 XX 29-JUL-1999; 99JP-00248036.  
 XX 27-AUG-1999; 99JP-00300253.  
 XX 11-JAN-2000; 2000JP-00118776.  
 XX 02-MAY-2000; 2000JP-00183767.  
 XX 09-JUN-2000; 2000JP-00241899.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI; 2001-318749/34.  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.  
 XX Claim 8; SEQ ID NO 17950; 2537pp + Sequence Listing; English.  
 XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH95893 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention  
 XX Sequence 431 AA;  
 Query Match 100.0%; Score 2211; DB 4; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPFGGSLTYTLVILCFILRLSASQNCCLKSLEDWIDIOSLSKIGRGNPEVYTSQ 60  
 DB 1 MPFGGSLTYTLVILCFILRLSASQNCCLKSLEDWIDIOSLSKIGRGNPEVYTSQ 60  
 QY 61 EDCINSCCTKNISGDKACNLMIFDTRKTARQNCYLFPCNBEACPLKPAKGLMSYRII 120  
 DB 61 EDCINSCCTKNISGDKACNLMIFDTRKTARQNCYLFPCNBEACPLKPAKGLMSYRII 120  
 QY 121 TDPPSLTRNLPSQELPQBSLLHGQFSQAVTPLAHHTDYSKPTDISWRDITLSQKFGSSD 180  
 DB 121 TDPPSLTRNLPSQELPQBSLLHGQFSQAVTPLAHHTDYSKPTDISWRDITLSQKFGSSD 180

QY 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSSQDOEIAHLLPENVSALPATVAVASPHTTSA 240  
 DB 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSSQDOEIAHLLPENVSALPATVAVASPHTTSA 240  
 QY 241 TPKPATLLPTNASVTPSGTSQPOLATTAPVTVTSQPPPTLLISTVFTTAAATLOAMATT 300  
 DB 241 TPKPATLLPTNASVTPSGTSQPOLATTAPVTVTSQPPPTLLISTVFTTAAATLOAMATT 300  
 QY 301 AVLTTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
 DB 301 AVLTTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
 QY 361 EASPGSSQSGVPENQYGLPFKWLIGSLLFGVLFVLVGLLGRILSESLEKRYSL 420  
 DB 361 EASPGSSQSGVPENQYGLPFKWLIGSLLFGVLFVLVGLLGRILSESLEKRYSL 420  
 QY 421 DYLINGIYVDI 431  
 DB 421 DYLINGIYVDI 431  
 RESULT 6  
 AAB65299 ID AAB65299 standard; protein; 431 AA.  
 XX AAB65299;  
 AC AC  
 XX 02-APR-2001 (first entry)  
 DT 02-APR-2001 (first entry)  
 XX Human PRO361 protein sequence SEQ ID NO:515.  
 KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX Homo sapiens.  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149396P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-MAR-2000; 2000WO-US005004.  
 PR 15-MAR-2000; 2000WO-US005841.  
 PR 20-MAR-2000; 2000WO-US006884.  
 XX 20-MAR-2000; 2000WO-US007377.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2001-032160/04.  
DR N-PSDB; AAF44268.  
XX PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX Claim 12; Fig 328; 935pp; English.  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytotstatic activity. The PRO proteins can  
XX be used for targeted delivery of bioactive molecules, such as toxins,  
XX radiolabels or antibodies, that cause cell death. PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes, in  
XX DNA. They may also be used to produce transgenic animals which are used  
XX to develop and screen therapeutically useful reagents. The PRO nucleotide  
XX and protein sequence can be used for tissue typing and in treating  
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
XX AAF4470 represent PCR primers and hybridisation probes used in the  
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
XX AAB65300 represent human PRO polynucleotide and protein sequences given  
XX in the exemplification of the present invention  
SQ Sequence 431 AA;  
Query Match 100.0%; Score 2211; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFFGEGSLTVLIIICPLTURLSASQCNLKKSLDVEDVVIDIQSSLKGIQNEPVTSTQ 60  
Db 1 MFFGEGSLTVLIIICPLTURLSASQCNLKKSLDVEDVVIDIQSSLKGIQNEPVTSTQ 60  
QY 61 EDCINSCSTKNSIGDKACNLMIFDTRKTARQPCNYLFFCNEACPLKPAKGLMSYRII 120  
Db 61 EDCINSCSTKNSIGDKACNLMIFDTRKTARQPCNYLFFCNEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLIRNLPFSQELPQEDSLHGFQSQAVTFLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
Db 121 TDFPSLIRNLPFSQELPQEDSLHGFQSQAVTFLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
QY 181 HLEKLFKMDASAQLLAYKERGHQSOSQFSSDQEIHAHLLPENVSALPATVAVASPHITSA 240  
Db 181 HLEKLFKMDASAQLLAYKERGHQSOSQFSSDQEIHAHLLPENVSALPATVAVASPHITSA 240  
QY 241 TPKPATLLPTNASVTPSGTSPQLATTAPPVTVTSQPTTLISTVFTRAAATLQAMATT 300  
Db 241 TPKPATLLPTNASVTPSGTSPQLATTAPPVTVTSQPTTLISTVFTRAAATLQAMATT 300  
QY 301 AVLTFTFOAPTDSKGSLETIPFTEISNLTGNYNPNFTALSMNSVESSTWNTKASMEGR 360  
Db 301 AVLTFTFOAPTDSKGSLETIPFTEISNLTGNYNPNFTALSMNSVESSTWNTKASMEGR 360  
QY 361 BASPGSSSQGVSPENQYGLPEKMLLIGSLFGVLVGLVILGRILSIRKRYSLR 420  
Db 361 BASPGSSSQGVSPENQYGLPEKMLLIGSLFGVLVGLVILGRILSIRKRYSLR 420  
QY 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431  
RESULT 7  
ABU55934  
ID ABU55934 standard; protein; 431 AA.  
XX  
AC ABU55934;  
XX  
DT 26-MAR-2003 (first entry)

XX Human secreted/transmembrane protein PRO361.  
DE Human; PRO; secreted protein; transmembrane protein; anti-HIV;  
XX cytotstatic; antiarteriosclerotic; antiinflammatory; antidiabetic;  
KW cardiant; AIDS; acquired immunodeficiency syndrome; cancer;  
KW atherosclerosis; inflammatory disease; diabetic complication;  
KW cardiac injury; organ failure.  
XX Homo sapiens.  
OS  
XX US2002142959-A1.  
XX 03-OCT-2002.  
XX 31-AUG-2001; 2001US-00944654.  
XX 16-SEP-1998; 98WO-US019330.  
XX 01-DEC-1998; 98WO-US025108.  
XX 22-JUN-1999; 99WO-US012252.  
XX 15-SEP-1999; 99WO-US021090.  
XX 30-NOV-1999; 99WO-US028313.  
XX 30-NOV-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 16-DEC-1999; 99WO-US030095.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 25-MAY-2001; 2001US-00866028.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX WPI; 2003-174141/17.  
DR N-PSDB; ABX75504.  
XX New isolated PRO polypeptide and encoding nucleic acid, useful for the  
PT diagnosis and treatment of disorders associated with the PRO polypeptide,  
PT such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.  
XX Claim 12; Fig 32; 178pp; English.  
XX The invention relates to an isolated PRO polypeptide (a secreted or  
XX transmembrane protein) comprising: (a) at least 80% sequence identity or  
XX positives when compared to any of 15 sequences, fully defined in the  
XX specification, lacking or with its associated signal peptide; or (b) at  
XX least 80% sequence identity to a sequence encoded by the full-length  
XX coding sequence of a DNA deposited in the American Type Culture  
XX Collection (ATCC). Also included are: (1) an isolated nucleic acid  
XX comprising: (a) at least 80% sequence identity to a nucleotide sequence  
XX that encodes a PRO protein; (b) at least 80% sequence identity to a  
XX nucleotide sequence or full-length coding sequence with any of 15 fully  
XX defined sequences of 957-3441 base pairs, given in the specification; or  
XX (c) at least 80% sequence identity to a full-length coding sequence of a  
XX DNA deposited under ATCC Accession No. 209526, 209508, 209524, 209528,  
XX 209530, 209523, 209492, 209532, 209531, 209529, 209527, 209570, 209618,  
XX 209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host  
XX cell comprising the vector which, when cultured under conditions suitable  
XX for expression of the PRO polypeptide, produces the PRO protein; (4) a  
XX chimeric molecule comprising PRO fused to a heterologous amino acid  
XX sequence; and (5) an anti-PRO antibody. The methods and compositions of  
XX the present invention are useful for the diagnosis and treatment of  
XX disorders associated with the PRO polypeptide, such as AIDS (acquired  
XX immunodeficiency syndrome), cancer, atherosclerosis, inflammatory  
XX disease, diabetic complications, cardiac injury and organ failure. The

CC antibodies can also be used in the different screening, therapeutic and  
 CC biological assays. The present sequence represents a PRO protein

XX Sequence 431 AA;  
 Query Match 100.0%; Score 2211; DB 6; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFPGGSGSLTYLVLIICFLTLRLSASQNCLEKSLSDVVIDIOSLSKGRGNEPVYTSQ 60  
 Db |||||  
 QY 61 EDCINSCCSTKNISGDKACNLMI FDKTKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
 Db |||||  
 QY 121 TDPPSLTRNLPSQELPQEDSLHLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
 Db |||||  
 QY 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSSDQEIHLHPENVSAIPATVAVASPHTTSA 240  
 Db |||||  
 QY 241 TPKPATLPTNASVTPSGTSQPOLATTPVTVTSQPTTLTISTVFTRAAATLQAMATT 300  
 Db |||||  
 QY 301 AVLTTFQAPTDSKGSLETIPETESNLNTGNVYNPTALSMNVESSTMNKTASWEGR 360  
 Db |||||  
 QY 361 EASPGSSQSGVPENQYGLPFPEKWLIIIGSLFLVGLVGLGRILSESRLRRRYRSL 420  
 Db |||||  
 QY 421 DYLINGIYVDI 431  
 Db |||||  
 RESULT 8  
 ABUS8114  
 ID ABUS8114 standard; protein; 431 AA.  
 XX  
 AC ABUS8114;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #146.  
 XX  
 KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ABEPI;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 US2003027163-A1.  
 PN  
 PD 06-FEB-2003.  
 XX  
 PF 15-NOV-2001; 2001US-00997666.  
 XX  
 PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-0088212P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088653P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088738P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088826P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088861P.  
 PR 11-JUN-1998; 98US-0088876P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089440P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 17-JUN-1998; 98US-0089538P.  
 PR 17-JUN-1998; 98US-0089598P.  
 PR 17-JUN-1998; 98US-0089599P.  
 PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089907P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 19-JUN-1998; 98US-0089947P.  
 PR 19-JUN-1998; 98US-0089948P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 22-JUN-1998; 98US-0090252P.  
 PR 22-JUN-1998; 98US-0090254P.  
 PR 23-JUN-1998; 98US-0090349P.  
 PR 23-JUN-1998; 98US-0090355P.  
 PR 24-JUN-1998; 98US-0090429P.  
 PR 24-JUN-1998; 98US-0090431P.  
 PR 24-JUN-1998; 98US-0090435P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 24-JUN-1998; 98US-0090445P.  
 PR 24-JUN-1998; 98US-0090472P.  
 PR 24-JUN-1998; 98US-0090535P.  
 PR 24-JUN-1998; 98US-0090540P.  
 PR 24-JUN-1998; 98US-0090542P.  
 PR 24-JUN-1998; 98US-0090557P.  
 PR 25-JUN-1998; 98US-0090676P.  
 PR 25-JUN-1998; 98US-0090678P.  
 PR 25-JUN-1998; 98US-0090690P.  
 PR 25-JUN-1998; 98US-0090694P.  
 PR 25-JUN-1998; 98US-0090695P.  
 PR 25-JUN-1998; 98US-0090696P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 26-JUN-1998; 98US-0090863P.  
 PR 01-JUL-1998; 98US-0091360P.  
 PR 01-JUL-1998; 98US-0091544P.  
 PR 02-JUL-1998; 98US-0091478P.  
 PR 02-JUL-1998; 98US-0091519P.  
 PR 02-JUL-1998; 98US-0091626P.  
 PR 02-JUL-1998; 98US-0091628P.

PR	02-JUL-1998;	98US-0091633P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-JUL-1998;	98US-0091646P.	PR	20-DEC-1999;	99WO-US030911.
PR	07-JUL-1998;	98US-0091673P.	PR	05-JAN-2000;	2000WO-US000219.
PR	07-JUL-1998;	98US-0091978P.	PR	06-JAN-2000;	2000WO-US000376.
PR	07-JUL-1998;	98US-0091982P.	PR	11-FEB-2000;	2000WO-US000365.
PR	09-JUL-1998;	98US-0092182P.	PR	18-FEB-2000;	2000WO-US000431.
PR	10-JUL-1998;	98US-0092472P.	PR	22-FEB-2000;	2000WO-US000414.
PR	20-JUL-1998;	98US-0093339P.	PR	24-FEB-2000;	2000WO-US0004914.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	2000WO-US005004.
PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095301P.	PR	10-MAR-2000;	2000WO-US006319.
PR	04-AUG-1998;	98US-0095302P.	PR	15-MAR-2000;	2000WO-US006884.
PR	04-AUG-1998;	98US-0095321P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095325P.	PR	30-MAR-2000;	2000WO-US008439.
PR	10-AUG-1998;	98US-0095929P.	PR	15-MAY-2000;	2000WO-US013358.
PR	10-AUG-1998;	98US-0096012P.	PR	17-MAY-2000;	2000WO-US013705.
PR	11-AUG-1998;	98US-0096143P.	PR	22-MAY-2000;	2000WO-US014042.
PR	11-AUG-1998;	98US-0096146P.	PR	30-MAY-2000;	2000WO-US014941.
PR	12-AUG-1998;	98US-0096329P.	PR	02-JUN-2000;	2000WO-US015264.
PR	17-AUG-1998;	98US-0096757P.	PR	23-JUN-2000;	2000US-0213637P.
PR	17-AUG-1998;	98US-0096766P.	PR	28-JUL-2000;	2000WO-US020710.
PR	17-AUG-1998;	98US-0096768P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096773P.	PR	23-AUG-2000;	2000WO-US023522.
PR	17-AUG-1998;	98US-0096791P.	PR	24-AUG-2000;	2000WO-US023328.
PR	17-AUG-1998;	98US-0096867P.	PR	07-SEP-2000;	2000US-0230978P.
PR	17-AUG-1998;	98US-0096891P.			
PR	17-AUG-1998;	98US-0096894P.			
PR	17-AUG-1998;	98US-0096895P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096949P.			
PR	18-AUG-1998;	98US-0096950P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0096960P.			
PR	19-AUG-1998;	98US-0097141P.			
PR	20-AUG-1998;	98US-0097218P.			
PR	24-AUG-1998;	98US-0097661P.			
PR	26-AUG-1998;	98US-0097952P.			
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0097979P.			
PR	26-AUG-1998;	98US-0097986P.			
PR	26-AUG-1998;	98US-0098014P.			
PR	31-AUG-1998;	98US-0098525P.			
PR	16-SEP-1998;	98US-0100634P.			
PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98US-0100858P.			
PR	17-SEP-1998;	98WO-US019437.			
PR	07-OCT-1998;	98WO-US021141.			
PR	01-DEC-1998;	98WO-US025108.			
PR	22-DEC-1998;	98US-0113298P.			
PR	05-JAN-1999;	99WO-US000106.			
PR	08-MAR-1999;	99WO-US005028.			
PR	12-MAR-1999;	99US-0123957P.			
PR	02-JUN-1999;	99WO-US012252.			
PR	23-JUN-1999;	98US-0141037P.			
PR	07-JUL-1999;	99US-0143048P.			
PR	20-JUL-1999;	99US-0144758P.			
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PR	17-AUG-1999;	99US-0149396P.			
PR	15-SEP-1999;	99WO-US021090.			
PR	15-SEP-1999;	99WO-US021547.			
PR	08-OCT-1999;	99US-0158663P.			
PR	30-NOV-1999;	99WO-US028313.			
PR	01-DEC-1999;	99WO-US028301.			
PR	01-DEC-1999;	99WO-US028634.			
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PR	07-JUL-1998;	98US-0091982P.	PR	11-FEB-2000;	2000WO-US000365.
PR	09-JUL-1998;	98US-0092182P.	PR	18-FEB-2000;	2000WO-US000431.
PR	10-JUL-1998;	98US-0092472P.	PR	22-FEB-2000;	2000WO-US000414.
PR	20-JUL-1998;	98US-0093339P.	PR	24-FEB-2000;	2000WO-US0004914.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	2000WO-US005004.
PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095301P.	PR	10-MAR-2000;	2000WO-US006319.
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PR	04-AUG-1998;	98US-0095321P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095325P.	PR	30-MAR-2000;	2000WO-US008439.
PR	10-AUG-1998;	98US-0095929P.	PR	15-MAY-2000;	2000WO-US013358.
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PR	17-AUG-1998;	98US-0096768P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096773P.	PR	23-AUG-2000;	2000WO-US023522.
PR	17-AUG-1998;	98US-0096791P.	PR	24-AUG-2000;	2000WO-US023328.
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PR	31-AUG-1998;	98US-0098525P.			
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PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98US-0100858P.			
PR	17-SEP-1998;	98WO-US019437.			
PR	07-OCT-1998;	98WO-US021141.			
PR	01-DEC-1998;	98WO-US025108.			
PR	22-DEC-1998;	98US-0113298P.			
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PR	08-MAR-1999;	99WO-US005028.			
PR	12-MAR-1999;	99US-0123957P.			
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PR	23-JUN-1999;	98US-0141037P.			
PR	07-JUL-1999;	99US-0143048P.			
PR	20-JUL-1999;	99US-0144758P.			
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PR	28-JUL-1999;	99US-0146222P.			
PR	17-AUG-1999;	99US-0149396P.			
PR	15-SEP-1999;	99WO-US021090.			
PR	15-SEP-1999;	99WO-US021547.			
PR	08-OCT-1999;	99US-0158663P.			
PR	30-NOV-1999;	99WO-US028313.			
PR	01-DEC-1999;	99WO-US028301.			
PR	01-DEC-1999;	99WO-US028634.			
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Db	1	MPFEGGSLTYTLVIICFLTLRLSASQNCCLKKSLEVDVIDIOSSLSKGRGNEPVTSTQ	60		
QY	61	EDCINSCCSTKNISGDKACNLMIFFDTRKTAROPNCYLFCPNEEACPLKPAKGLMSYRII	120		
Db	61	EDCINSCCSTKNISGDKACNLMIFFDTRKTAROPNCYLFCPNEEACPLKPAKGLMSYRII	120		
QY	121	TDPPSLTRNLPSQELPQEDSLHGFQSQVATPLAHHTDYSKPTDISWRDTLSQKFGSSD	180		
Db	121	TDPPSLTRNLPSQELPQEDSLHGFQSQVATPLAHHTDYSKPTDISWRDTLSQKFGSSD	180		
QY	181	HLEKLFKMEASQAOLLAAYKEKHSQSSQSFSSDQEIHLHPENVSALPATVAVASPHTTSA	240		
Db	181	HLEKLFKMEASQAOLLAAYKEKHSQSSQSFSSDQEIHLHPENVSALPATVAVASPHTTSA	240		
QY	241	TPKPATLLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLQAMATT	300		
Db	241	TPKPATLLPTNASVTPSGTSQPOLATTAPVTTVTSQPTTLISTVFTRAAATLQAMATT	300		
QY	301	AVLTTFQAPTDKSGSLTIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR	360		
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QY	361	EASPGSSQSGSVENQYGLPPEKWLIGSLFGVLVIGLVLLGRILTSLSLRKRYSL	420		
Db	361	EASPGSSQSGSVENQYGLPPEKWLIGSLFGVLVIGLVLLGRILTSLSLRKRYSL	420		
QY	421	DYLINGIYVDI	431		
Db	421	DYLINGIYVDI	431		
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ABUS9192					
ID ABUS9192 standard; protein; 431 AA.					
XX ABUS9192;					
XX AC					
XX 28-APR-2003 (first entry)					
XX Novel human secreted or transmembrane protein PRO361.					
XX					

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.

XX Homo sapiens.

XX US2002132252-A1.

XX 19-SEP-2002.

XX 14-NOV-2001; 2001US-0090442.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0065770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-0087609P.

XX 02-JUN-1998; 98US-0087759P.

XX 03-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

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XX 05-JUN-1998; 98US-0088212P.

XX 05-JUN-1998; 98US-0088217P.

XX 09-JUN-1998; 98US-0088555P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088738P.

XX 10-JUN-1998; 98US-0088742P.

XX 10-JUN-1998; 98US-0088810P.

XX 10-JUN-1998; 98US-0088824P.

XX 10-JUN-1998; 98US-0088826P.

XX 11-JUN-1998; 98US-0088858P.

XX 11-JUN-1998; 98US-0088861P.

XX 11-JUN-1998; 98US-0088876P.

XX 12-JUN-1998; 98US-0089105P.

XX 16-JUN-1998; 98US-0089440P.

XX 16-JUN-1998; 98US-0089512P.

XX 16-JUN-1998; 98US-0089513P.

XX 17-JUN-1998; 98US-0089532P.

XX 17-JUN-1998; 98US-0089538P.

XX 17-JUN-1998; 98US-0089598P.

XX 17-JUN-1998; 98US-0089599P.

XX 17-JUN-1998; 98US-0089600P.

XX 17-JUN-1998; 98US-0089653P.

XX 18-JUN-1998; 98US-0089801P.

XX 18-JUN-1998; 98US-0089907P.

XX 18-JUN-1998; 98US-0089908P.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

XX 07-OCT-1998; 98WO-US021141.

XX 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
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 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
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 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
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 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gorrissen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI; 2003-247083/24.  
 XX N-PSDB; ABX80473.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 are therapeutically useful for enhancing immune response and in cancer  
 treatments.

XX Claim 12; Fig 328; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 polypeptides are useful in detecting PRO polypeptides in a sample, in  
 linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 in modulating at least one biological activity of a cell expressing a PRO  
 polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 useful for treating conditions or disorders where angiogenesis would be  
 beneficial, e.g. wound healing and antagonist of this polypeptide are  
 useful for treating cancerous tumours. PRO812 inhibits vascular  
 endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 cells and is thus useful for inhibiting endothelial cell growth in  
 mammals which would be beneficial in inhibiting tumour growth. PRO826,



CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein  
XX Sequence 431 AA;  
SQ

Query Match 100.0%; Score 2211; DB 6; Length 431;  
Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFGGEGSLYTVIIICFLIRLSASQNCCLKSLEDVVIDIQSSLKGIRGNEPVTSTQ 60

Qy 61 EDCINCCSTKNISGDKACNLMIFDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
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Qy 121 TDFPSLTRNLPSQELPOEDSLHGFQSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
Db 121 TDFPSLTRNLPSQELPOEDSLHGFQSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180

Qy 181 HLEKLFQWDEASAOQLLAYKKGHSQSQSFSDQSDOBIAHLLENVSALPATVAVASPHHTSA 240  
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Qy 241 TPKPATLLPTNASVTPSGTSPQALATTAPVTVTTTSQPTTLTSTVETRAAATLQAWATT 300  
Db 241 TPKPATLLPTNASVTPSGTSPQALATTAPVTVTTTSQPTTLTSTVETRAAATLQAWATT 300

Qy 301 AVLTFTTQAPDTSKGSLETIPFTFISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGR 360  
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Qy 361 EASPGSSSQSVENQYGLPFKEKWLIGSLFLGVFLVIGLVILGRILSELRRKYSRL 420  
Db 361 EASPGSSSQSVENQYGLPFKEKWLIGSLFLGVFLVIGLVILGRILSELRRKYSRL 420

Qy 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431

RESULT 10  
ABU82704  
ID ABU82704 standard; protein; 431 AA.  
XX AC ABU82704;  
XX DT 26-JUN-2003 (first entry)  
XX DE Human secreted/transmembrane protein PRO361.  
XX KW Human; PRO; secreted protein; transmembrane protein;  
KW cardiac insufficiency disorders; angiogenesis; wound healing;  
KW cancerous tumour; immune response; retinal disorder; sight loss;  
KW retinitis pigmentosa; age-related macular degeneration; AMD;  
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;  
KW Crohn's disease; sports injury; arthritis.  
XX OS Homo sapiens.  
XX

PN US2003032023-A1.  
XX 13-FEB-2003.  
XX 14-NOV-2001; 2001US-00990711.  
XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
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PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
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PR 23-JUN-1998; 98US-0090355P.  
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PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090542P.



PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
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PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
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PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 12-AUG-1998; 98US-0096323P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 19-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098523P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98US-0100858P.  
PR 07-OCT-1998; 98US-0100914P.  
PR 01-DEC-1998; 98US-0100914P.  
PR 22-DEC-1998; 98US-0100914P.  
PR 05-JAN-1999; 98US-0100914P.

PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-JUN-2000; 2000US-0213637P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 2211; DB 6; Length 431;  
Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGEGSLTVLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGRGNEPYVTSTQ 60  
DB 1 MFFGEGSLTVLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGRGNEPYVTSTQ 60  
QY 61 EDCINSCCSTKNIISGDKACNLMI FDTKTRARQPCNLCYLFPCNEEACPLKPAKGLMSYRII 120  
DB 61 EDCINSCCSTKNIISGDKACNLMI FDTKTRARQPCNLCYLFPCNEEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLTRLNLPSELPOEDSLLHGQFQSOAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
DB 121 TDFPSLTRLNLPSELPOEDSLLHGQFQSOAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
QY 181 HLEKLFKMDSEASQALLAYKEGHSQSSQFSSQSDQIEAHLHPNVSPALPATVAVASPHTTSA 240  
DB 181 HLEKLFKMDSEASQALLAYKEGHSQSSQFSSQSDQIEAHLHPNVSPALPATVAVASPHTTSA 240  
QY 241 TPKPATLLPTNASVTPSGTSQPLATTPVTTVTSQPTTLISTVFTTAAATLOAMATT 300  
DB 241 TPKPATLLPTNASVTPSGTSQPLATTPVTTVTSQPTTLISTVFTTAAATLOAMATT 300  
QY 301 AVLTTTFOAPTDSKGSLETTIPFTISNLTNTGNVYNTALSMNSVESSTWNTKASWGR 360  
DB 301 AVLTTTFOAPTDSKGSLETTIPFTISNLTNTGNVYNTALSMNSVESSTWNTKASWGR 360  
QY 361 EASFGSSSQSVENQYGLPFKWLIGSLFGVLFLVGLVLLGRILSESILRRKRYSL 420  
DB 361 EASFGSSSQSVENQYGLPFKWLIGSLFGVLFLVGLVLLGRILSESILRRKRYSL 420  
QY 421 DYLINGIYVDI 431  
DB 421 DYLINGIYVDI 431

RESULT 11  
ABU0623  
ID ABU0623 standard; protein; 431 AA.  
XX  
XX  
AC ABU0623;  
XX  
XX  
DT 01-MAY-2003 (first entry)  
XX  
XX  
DE Human secreted/transmembrane protein, #182.  
XX  
XX  
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
KW diagnostic; therapeutic; gene therapy.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2002160384-A1.  
XX  
XX  
PD 31-OCT-2002.  
XX  
XX  
PF 14-NOV-2001; 2001US-00992598.  
XX  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 05-JUN-1998; 98US-0088255P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088866P.  
PR 12-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089603P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 18-JUN-1998; 98US-0089909P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US000376.  
PR 18-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004341.  
PR 24-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 10-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 20-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US007377.  
PR 15-MAY-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013358.  
PR 22-MAY-2000; 2000WO-US013705.  
PR 30-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US014941.  
PR 28-JUL-2000; 2000WO-US015264.  
PR 11-AUG-2000; 2000WO-US020710.  
PR 23-AUG-2000; 2000WO-US022031.  
PR 24-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US030952.  
PR 28-FEB-2001; 2000WO-US032678.  
PR 01-JUN-2001; 2001WO-US006520.  
PR 20-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001WO-US019692.  
PR 09-JUL-2001; 2001WO-US021066.  
PR 28-AUG-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX  
DR WFI; 2003-288106/28.  
DR N-PSDB; ABX90451.  
XX  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes.  
XX  
XX  
PS Claim 12; Fig 328; 650pp; English.  
XX  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or  
CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein electrophoresis,  
CC and the isolated nucleic acids may be used for recombinantly expressing  
CC those markers. The PRO polypeptides and nucleic acids may also be used in  
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

CC PRO, and in affinity purification of PRO from recombinant cell culture or  
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC is also available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;  
Best Local Similarity 100.0%; Pred. NO. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGEGSITVTLVITICFTRLSASQNCCKSLKLEWDVIOSSLSKGRGNEPVYTSQ 60  
Db 1 MFFGEGSITVTLVITICFTRLSASQNCCKSLKLEWDVIOSSLSKGRGNEPVYTSQ 60  
QY 61 EDCINSCCKTNIISGDKACNLMIFDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
Db 61 EDCINSCCKTNIISGDKACNLMIFDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLTRNLPQELPQEDSLRHGFQSQVTPLAHHHTDYSKPTDISWRDITLSQKFGSSD 180  
Db 121 TDFPSLTRNLPQELPQEDSLRHGFQSQVTPLAHHHTDYSKPTDISWRDITLSQKFGSSD 180  
QY 181 HLEKLFKMDASAQILAYKEKGHSOSSQFSSDOETIAHLLPENVSALPATVAVASPHITSA 240  
Db 181 HLEKLFKMDASAQILAYKEKGHSOSSQFSSDOETIAHLLPENVSALPATVAVASPHITSA 240  
QY 241 TPKPATLLPTNASVTPSGTSQPOLATTPPVTTVTSQPTTLITSTVETRAATLQAMATT 300  
Db 241 TPKPATLLPTNASVTPSGTSQPOLATTPPVTTVTSQPTTLITSTVETRAATLQAMATT 300  
QY 301 AVLTTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWGR 360  
Db 301 AVLTTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWGR 360  
QY 361 EASPGSSQSGVPENQYGLPEKWLILGSLFLGVLFVIGLVILGRILSESILRRKRYSL 420  
Db 361 EASPGSSQSGVPENQYGLPEKWLILGSLFLGVLFVIGLVILGRILSESILRRKRYSL 420  
QY 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431

## RESULT 12

ABU14005  
ID ABU14005 standard; protein; 431 AA.  
XX  
AC ABU14005;  
XX  
XX  
DT 26-FEB-2003 (first entry)  
XX  
XX  
DE Human PRO361 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive.  
XX  
XX Homo sapiens.  
XX  
FN US2002103125-A1.  
XX  
XX  
PD 01-AUG-2002.  
XX  
PF 20-NOV-2001; 2001US-00989731.  
XX

PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065185P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.



PR	30-MAR-2000;	2000WO-US008439.
PR	22-MAY-2000;	2000WO-US014042.
PR	28-JUL-2000;	2000WO-US020710.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-FEB-2001;	2001WO-US006520.
PR	25-MAY-2001;	2001US-00866028.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;	
PI	Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;	
PI	Hillman KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;	
XX		
DR	WPI; 2003-174088/17.	
DR	N-PSDB; ABX89495.	
XX		
PT	New secreted and transmembrane polypeptides (e.g. PRO241, for use in	
PT	pharmaceuticals, diagnostics or bioreactors, particularly for detecting	
PT	or treating e.g. cancers, infertility or acquired immunodeficiency	
PT	syndrome in mammals.	
XX		
PS	Claim 1; Fig 32; 173pp; English.	
XX		
CC	The invention relates to a human secreted and transmembrane polypeptide	
CC	(PRO) and the polynucleotide encoding it. The PRO polypeptide or	
CC	polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or	
CC	bioreactors. These are particularly useful for detecting or treating	
CC	cancers, inflammatory diseases, atherosclerosis, cardiac injury,	
CC	infertility, birth defects, premature aging, acquired immunodeficiency	
CC	syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,	
CC	cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are	
CC	also useful in biotechnological and medical research and in various	
CC	industrial applications. Sequences ABU60230-ABU60245 represent human PRO	
CC	polypeptides of the invention	
XX		
SQ	Sequence 431 AA;	
	Query Match	
	Best Local Similarity 100.0%; Score 2211; DB 6; Length 431;	
	Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MFFGEGSLTYTLVLCITLRLSASQCLKSLDVIDIQLSSKLGIRGNEPVYTSTQ 60	
DB	1 MFFGEGSLTYTLVLCITLRLSASQCLKSLDVIDIQLSSKLGIRGNEPVYTSTQ 60	
QY	61 EDCINSCSTKNI SGDKACNLMI FTRKTARQPCVLCFPCNEEACPLKPKGLMSYRII 120	
DB	61 EDCINSCSTKNI SGDKACNLMI FTRKTARQPCVLCFPCNEEACPLKPKGLMSYRII 120	
QY	121 TDFPSLTRNLPSQELPQEDSLHGFQSOAVTFLAHHHTDYSKPTDISWRDTLSQKFGSSD 180	
DB	121 TDFPSLTRNLPSQELPQEDSLHGFQSOAVTFLAHHHTDYSKPTDISWRDTLSQKFGSSD 180	
QY	181 HLEKLFKMDASAQLLAYKEKHGSSQSFSSDQETIAHLLPENVSALPATVAVASPHHTSA 240	
DB	181 HLEKLFKMDASAQLLAYKEKHGSSQSFSSDQETIAHLLPENVSALPATVAVASPHHTSA 240	
QY	241 TPKPATLPTNASVTPSGTSPQLATTAPPVTVTSQBPPTTLISTVFTRAAATLQAMATT 300	
DB	241 TPKPATLPTNASVTPSGTSPQLATTAPPVTVTSQBPPTTLISTVFTRAAATLQAMATT 300	
QY	301 AVLTFTFOAPTDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTWNTKTSWEGR 360	
DB	301 AVLTFTFOAPTDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTWNTKTSWEGR 360	
QY	361 EASPGSSQGVSPENQYGLPEKMLLIGSLFGVLFLVIGLVLLGRILSESILRRKYSRL 420	
DB	361 EASPGSSQGVSPENQYGLPEKMLLIGSLFGVLFLVIGLVLLGRILSESILRRKYSRL 420	
QY	421 DYLINGIYVDI 431	
DB	421 DYLINGIYVDI 431	

RESULT 14

ABU72590

ID ABU72590 standard; protein; 431 AA.

XX

AC ABU72590;

XX

DT 17-JUN-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO361.

XX

KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;

KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;

KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;

KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;

KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;

KW drug screening.

XX

OS Homo sapiens.

XX

PN US2003003531-A1.

XX

PD 02-JAN-2003.

XX

PF 19-NOV-2001; 2001US-00989734.

XX

PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089440P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089599P.

PR 17-JUN-1998; 98US-0089600P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089807P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 (GETH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-352829/33.  
 DR N-PSDB; ACA64519.  
 XX  
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
 PT disease.  
 XX Claim 12; Fig 328; 663pp; English.  
 PS  
 XX The invention describes a new isolated nucleic acid molecule comprising  
 CC the full length coding sequence of the DNA deposited with the American  
 CC Type Culture Collection (e.g. ATCC deposit No. 209621, 552-PTA, 819-PTA,  
 CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA  
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
 CC are particularly useful for detecting or treating e.g. malignancies or  
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,

CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
 CC disease in mammals. The PRO polypeptides are useful in drug screening,  
 CC particularly as targets for therapeutic intervention in these diseases,  
 CC and in the diagnostic determination of the presence of these diseases.  
 CC The PRO polypeptides are also useful as molecular weight markers, or for  
 CC chromosome identification. The PRO genes are useful as hybridisation  
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
 CC The PRO genes may also be used in gene therapy, particularly for  
 CC replacing a defective gene. This is the amino acid sequence of a novel  
 CC human secreted and transmembrane PRO polypeptide  
 XX  
 SQ Sequence 431 AA;

Query Match 100.0%; Score 2211; DB 6; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
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 QY 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCNYLFCPNEEACPLKPKGLMSYRII 120  
 DB 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCNYLFCPNEEACPLKPKGLMSYRII 120  
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 DB 181 HLEKLFKMDASAQLLAYKEKHSQSQSFSSDQEIHLHPENVSALPATVAVASPHTTSA 240  
 QY 241 TPXPATILLPTNASVTPSGTSOPOLATTAPPVTTTSOPPTLLISTVFTRAAATLQAWATT 300  
 DB 241 TPXPATILLPTNASVTPSGTSOPOLATTAPPVTTTSOPPTLLISTVFTRAAATLQAWATT 300  
 QY 301 AVLTTFQAPTDKSGSLETPFTEISNLTNTGNVNTALSNVSNVESSTMNKTASWEGR 360  
 DB 301 AVLTTFQAPTDKSGSLETPFTEISNLTNTGNVNTALSNVSNVESSTMNKTASWEGR 360  
 QY 361 EASPGSSSQGVPEVNYGLPFKEKWLIGSLFGVLFVLGLVLLGRILSSSLRKRYSRL 420  
 DB 361 EASPGSSSQGVPEVNYGLPFKEKWLIGSLFGVLFVLGLVLLGRILSSSLRKRYSRL 420  
 QY 421 DYLINGIYVDI 431  
 DB 421 DYLINGIYVDI 431

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 ID ABUS4930 standard; protein; 431 AA.  
 XX AC ABUS4930;  
 XX DT 15-MAY-2003 (first entry)  
 XX DE Human secreted/transmembrane protein PRO361.  
 XX KW Human; PRO; secreted protein; transmembrane protein;  
 XX KW Cornelia de Lange syndrome; gene therapy; immune disorder;  
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;  
 KW diabetic complication.  
 XX OS Homo sapiens.  
 XX PN US2002173463-A1.  
 XX PD 21-NOV-2002.  
 XX PF 31-AUG-2001; 2001US-00944944.

CC AIDS, cancer and diabetic complications. The present sequence represents  
CC a PRO protein  
XX  
SQ Sequence 431 AA;  
Query Match 100.0%; Score 2211; DB 6; Length 431;  
Best Local Similarity 100.0%; Pred. No. 4.9e-173;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MFFGEGSLTYTLVIICFLTLRLSASQNLKSLKSLDWDVVIDIQSSLSKIGRGNPEVYTSQ 60  
QY 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFCFPCNEEACPLKPAKGLMSYRII 120  
DB 61 EDCINSCCSTKNISGDKACNLMI FTRKTARQPCNYLFCFPCNEEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLTENLPSQELPOEDSLHGOFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
DB 121 TDFPSLTENLPSQELPOEDSLHGOFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
QY 181 HLEKLFKMDASAQLLAYKEGHSQSOFSSDQELAHLLPENVSALPATVAVASPHITSA 240  
DB 181 HLEKLFKMDASAQLLAYKEGHSQSOFSSDQELAHLLPENVSALPATVAVASPHITSA 240  
QY 241 TPKPATLLPTNASVTPSGTSQPLATTAPPVTTVTSQPPPTTLISTVFTRAAATLQAMATT 300  
DB 241 TPKPATLLPTNASVTPSGTSQPLATTAPPVTTVTSQPPPTTLISTVFTRAAATLQAMATT 300  
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DB 301 AVLTTFQAPTDSKGSLETIPFTEISNLTATGNVYNPTALSMNSVESTWNKTASWEGR 360  
QY 361 EASPGSSSQSVPENQYGLPPEKWLIGSLFGVLFLVIGLVLLGRILSESURRKYRSL 420  
DB 361 EASPGSSSQSVPENQYGLPPEKWLIGSLFGVLFLVIGLVLLGRILSESURRKYRSL 420  
QY 421 DYLINGIYVDI 431  
DB 421 DYLINGIYVDI 431

Search completed: April 26, 2005, 21:49:17  
Job time : 129 secs

XX 03-DEC-1997; 97US-0067411P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 16-DEC-1997; 97US-0069696P.  
PR 16-DEC-1997; 97US-0069702P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 05-JAN-1998; 98US-0070440P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 16-DEC-1998; 98US-0112850P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 28-JUL-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kljavin LJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX  
DR WPI; 2003-311003/30.  
DR N-PSDB; ABX96832.  
XX  
PT New transmembrane polypeptides and polynucleotides useful for chromosome  
PT identification, tissue typing, gene therapy, in chromosome and gene  
PT mapping, or as molecular weight markers.  
XX  
PS Claim 12; Fig 32; 172pp; English.  
XX  
CC The invention relates to an isolated nucleic acid encoding a secreted/  
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO  
CC polypeptides and their encoding polynucleotides are disclosed. Also  
CC included are a vector comprising the PRO nucleic acid, a host cell  
CC comprising the vector, a process for producing a PRO polypeptide (by  
CC culturing the host cell under conditions for the expression of the PRO  
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an  
CC isolated polypeptide having at least 80% amino acid sequence identity to  
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a  
CC heterologous amino acid sequence and an antibody which specifically binds  
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,  
CC in chromosome and gene mapping, in generating sense and antisense RNA or  
CC DNA, in generating transgenic or knock-out animals which can be used in  
CC the development and screening of therapeutically useful reagents, and in  
CC gene therapy. The polypeptides may be used as molecular weight markers  
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic  
CC acids may also be used for chromosome identification and tissue typing.  
CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange  
CC syndrome. Other PRO proteins are variously implicated in immune  
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac  
CC injury, infertility, birth defects, premature aging, cardiac injury,

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GenCore version 5.1.6  
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QM protein - protein search, using sw model

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(without alignments)  
584.977 Million cell updates/sec

Title: US-10-735-014-83  
Perfect score: 2211  
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Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	149.5	6.8	5179	4	US-09-538-092-1258
5	145.5	6.6	629	3	US-09-241-581B-6
6	145.5	6.6	629	4	US-08-265-428-6
7	145.5	6.6	629	5	PCT-US95-07721-6
8	144.5	6.5	1140	4	US-09-538-092-647
9	136	6.2	2870	4	US-09-479-467A-15
10	136	6.2	3178	4	US-09-479-467A-4
11	133	6.0	556	4	US-09-538-092-712
12	132	6.0	788	4	US-09-294-663-3
13	132	6.0	807	4	US-09-294-663-4
14	129	5.8	175	3	US-08-700-651-12
15	129	5.8	175	3	US-08-928-361B-17
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17	128	5.8	249	3	US-08-700-651-15
18	128	5.8	249	3	US-08-928-361B-20
19	128	5.8	249	4	US-09-588-995A-20
20	128	5.8	870	4	US-09-538-092-77
21	127.5	5.8	1601	4	US-09-345-473E-40
22	127	5.7	288	4	US-09-216-393B-341
23	127	5.7	288	4	US-09-216-393B-344
24	127	5.7	357	1	US-08-078-683A-8
25	127	5.7	357	4	US-08-471-970A-8
26	127	5.7	357	4	US-08-723-677B-8
27	126.5	5.7	1837	3	US-08-928-361B-5

28	126.5	5.7	1837	4	US-09-588-995A-5	Sequence 5, Appli
29	126	5.7	878	4	US-09-556-706B-2	Sequence 2, Appli
30	126	5.7	878	4	US-09-724-418A-2	Sequence 2, Appli
31	125.5	5.7	1721	3	US-08-700-651-5	Sequence 5, Appli
32	125.5	5.7	1721	3	US-08-928-361B-6	Sequence 6, Appli
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37	124.5	5.6	1306	4	US-09-538-092-330	Sequence 330, App
38	124	5.6	827	4	US-09-248-796A-17307	Sequence 17307, A
39	123.5	5.6	638	4	US-09-248-796A-18750	Sequence 18750, A
40	123.5	5.6	806	1	US-08-270-076A-11	Sequence 11, Appl
41	123	5.6	150	3	US-08-928-361B-18	Sequence 18, Appl
42	123	5.6	150	4	US-09-588-995A-18	Sequence 18, Appl
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44	123	5.6	334	4	US-09-197-970B-7	Sequence 7, Appli
45	122.5	5.5	542	4	US-09-538-092-289	Sequence 289, App

ALIGNMENTS

RESULT 1  
US-09-866-028-83  
; Sequence 83, Application US/09866028  
; Patent No. 6642360  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/866,028  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 83  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-866-028-83

Query Match	100.0%;	Score	2211;	DB	4;	Length	431;
Best Local Similarity	100.0%;	Pred. No.	2.9e-202;	Mismatches	0;	Indels	0;
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Db	1	MFPGGGSITVLIICFLTLRLSASQNCLEKSLDWDVDIQSSLSKGRGNEPVYTSTQ	60				
QY	61	EDCINSCCSTKNIISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII	120				
Db	61	EDCINSCCSTKNIISGDKACNLMI FTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRII	120				
QY	121	TDFPSLTNLPSQELPOEDSLHGFQSAVTPPLAHHHTDYSKPTDISWDTLSQKFGSSD	180				
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DB 361 EASGSSSSQGVNPOYGLPEKWLIGSLFGVLFLVIGLVLGRILSLSLRKRYRSL 420  
QY 421 DYLLINGIYVDI 431  
DB 421 DYLLINGIYVDI 431

RESULT 2  
US-09-944-457-83  
; Sequence 83, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548PICI  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866, 028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067, 411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068, 017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070, 440  
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074, 086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074, 092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075, 945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112, 850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113, 296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146, 222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216, 021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218, 517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254, 311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 83  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-457-83

Query Match 100.0%; Score 2211; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.9e-202; Indels 0; Gaps 0;  
Matches 431; Conservative 0; Mismatches 0

QY 1 MFFGEGSLTYTLVVICFLTLRLSASQNCCKLSLEDVVVDIQSSLSKIGRNEPVYTSTQ 60  
DB 1 MFFGEGSLTYTLVVICFLTLRLSASQNCCKLSLEDVVVDIQSSLSKIGRNEPVYTSTQ 60  
QY 61 EDCINSCCSTKNISGDKACNLMIEDTRKTRQPNCYLFFCCNEEACPLKPAKGLMSYRII 120  
DB 61 EDCINSCCSTKNISGDKACNLMIEDTRKTRQPNCYLFFCCNEEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLTNLPQSQELPQEDSLHGFQSOAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180  
DB 121 TDFPSLTNLPQSQELPQEDSLHGFQSOAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180

QY 181 HLEKLFKMDDEAQAQLLAYKEKHSOSSQSSDOEIAHLLPENVSALPATVAVASPHTTSA 240  
DB 181 HLEKLFKMDDEAQAQLLAYKEKHSOSSQSSDOEIAHLLPENVSALPATVAVASPHTTSA 240  
QY 241 TPKPATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLLISTVFTRAAATLQAMATT 300  
DB 241 TPKPATLLPTNASVTPSGTSQPOLATAPPVTTVTSQPTTLLISTVFTRAAATLQAMATT 300  
QY 301 AVLTTFQAPDTSKGSLETIPTEISNLTNTGNVNPPTALSMSNVESSTMNKTASWEGR 360  
DB 301 AVLTTFQAPDTSKGSLETIPTEISNLTNTGNVNPPTALSMSNVESSTMNKTASWEGR 360  
QY 361 EASPGSSSGSVPEVQYGLPFKFKWLLIGSLFGVLFLVIGLVLLGRILSESRLRRYRSL 420  
DB 361 EASPGSSSGSVPEVQYGLPFKFKWLLIGSLFGVLFLVIGLVLLGRILSESRLRRYRSL 420  
QY 421 DYLLINGIYVDI 431  
DB 421 DYLLINGIYVDI 431

RESULT 3  
US-09-847-332  
; Sequence 332, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; FILE REFERENCE: P2031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; EARLIER FILING DATE: 2000-01-24  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 332  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (97)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (174)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (195)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (199)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (206)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-489-847-332  
Query Match 8.3%; Score 183; DB 4; Length 266;  
Best Local Similarity 27.2%; Pred. No. 5e-09;

Matches 80; Conservative 42; Mismatches 116; Indels 56; Gaps 13;  
QY 158 TDYKPTDISMRDTSKQSGSDHLEKLFKMDDEAQAQLLAYKEKHSOSSQSSDOEIAH 217  
DB 5 TEDISSRTDVSSEPATSG--GAADGVTSTIAPTAVASSTTAA-----SITTAASSMTVAS 54  
QY 218 LLPENVSALPATVAVASPHTT-----TSATPKPATL-LPTNASV-----TPS--GTSOPOLA 265  
DB 55 SAP-TTAAASSTTVASIAPTTTTASSMTAAASSTPMTLALPAPTSTXTGRTPTTATGHPSL 113  
QY 266 TTAPVTTVTSQPTTLLISTVFTRAAATLQAMATTAVLTTFQA-PTDSKGSLETIPFTE 324  
DB 114 TALAQVPKSSALPRATLATLATRA----QIVAITANTSSPMSTPSPSKHMPSDTAASP 169  
QY 325 ISNLTNTGNVNPPTA---LSMSNVESSTMNKTASWEGREASPGSSSGSVPEVQYGLPF 381  
DB 170 VPPMX-----POAQGPISQSVDPVWNTT-----XKSTXMPSTNTXEP 209  
QY 382 -----EKWLLIGSLFGVLFLVIGLVLLGRILSESRLRRYRSLRDYLLINGIYVD 430  
DB 210 TQAVVDKTLVLLVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLLINGMYAD 263

RESULT 4  
US-09-538-092-1258  
; Sequence 1258, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqFormatter Version 0.9  
; SEQ ID NO 1258  
; LENGTH: 5179  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (0)---(0)  
; OTHER INFORMATION: Polypeptide Accession Number Q02817  
US-09-538-092-1258

Query Match 6.8%; Score 149.5; DB 4; Length 5179;  
Best Local Similarity 34.1%; Pred. No. 0.00095;  
Matches 43; Conservative 12; Mismatches 52; Indels 19; Gaps 4;  
QY 220 PENVSALPATVAVASPHTTSATPKPATL-LPTNASVTP--SGTSOPOLATAPPVTTVT 275  
DB 1511 PASTTTLPPTTPSPPTTTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTT 1570  
QY 276 SQPTTLLIS-----TVFTRAAATLQAMATTAVLTTFQAPTDSKGSLETIPFT 323  
DB 1571 TPTTTPPTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTT 1627  
QY 324 EISNLT 329  
DB 1628 PPTSTT 1633  
; RESULT 5  
US-09-241-581B-6  
; Sequence 6, Application US/09241581B  
; Patent No. 6350859  
; GENERAL INFORMATION:  
; APPLICANT: Massachusetts Institute of Technology

```

; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241.581B
; FILING DATE: 02-Feb-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 629 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 1..629
; OTHER INFORMATION: /Function = "Amino acid sequence for the
; Drosophila Melanogaster Scavenger Receptor
; Class CI."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 30..353
; OTHER INFORMATION: /note= "Positions 30-32, 90-92,
; 129-131, 180-182, 253-255 and 351-353
; represent potential N-glycosylation
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..20
; OTHER INFORMATION: /note= "Amino acids 1-20 represent
; a putative signal sequence."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21..74
; OTHER INFORMATION: /note= "Amino acids 21-74 represent
; complement control protein domain
; number 1."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 75..127
; OTHER INFORMATION: /note= "Amino acids 75-127
; represent complement control protein
; domain number 2."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 128..312
; OTHER INFORMATION: /note= "Amino acids 128-312
; represent an MAM domain."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 22..381
; OTHER INFORMATION: /note= "The cysteines at positions

```

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; 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216,
; 217, 254, 310, 339, 343, 361, 363, 367, 373, 374
; and 381 represent potential disulfide linkages."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 338..381
; OTHER INFORMATION: /note= "Amino acids 338-381
; represent a somatomedin B domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 387..514
; OTHER INFORMATION: /note= "Amino acids 387-514
; represent a mucin-like potential
; O-linked glycosylation region."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 544..564
; OTHER INFORMATION: /note= "Amino acids 544-565
; represent a putative TM domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 565..629
; OTHER INFORMATION: /note= "Amino acids 565-629
; represent a putative cytoplasmic
; domain."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 576..602
; OTHER INFORMATION: /note= "Amino acids 576-579 and
; 599-602 represent casein kinase II
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 578..592
; OTHER INFORMATION: /note= "Amino acids 578-580 and
; 590-592 represent protein kinase C
; sites."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 596..599
; OTHER INFORMATION: /note= "Amino acids 596-599
; represent a CAMP protein kinase site."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-09-241-581B-6
;
; Query Match 6.8%; Score 145.5; DB 3; Length 629;
; Best Local Similarity 22.9%; Pred. No. 7.6e-05;
; Matches 48; Conservative 30; Mismatches 79; Indels 53; Gaps 5;
;
; QY 213 QETAHLLPENVSALPATVAVASPHI-----TSATPKPATLLPTNASVTPSGTSQ 261
; Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
; 383 KELLTTEDDISLPPTVSTSTSTTRKSTTTTSTTTTSTTTTSTTTTSTTTTSTTTTSTTTT 442
; QY 262 POLATTAPPVTVTSQPTTLISTVTFRAATLQAMATTAVALTTTFOAPDTSKGSLETIP 321
; Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
; 443 KRITTTKKPTTSTTPKPTTSTTPKSTTSTTSTTSTTSTTSTTSTTSTTSTTSTTSTTSTT 495
; QY 322 FTEISNLTNTGNVNPALTSMNSVSSSTMNKTSW-----EGREASPGSSSSQGSVPE 374
; Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
; 496 -----TTIMPTSTSTKTTGI-----ITMTKTKKITWNVDPDIEGHMDTSGSTPNPALV- 546
; QY 375 NQYGLPKKLLIGSLFGVLFVLVIGLVLL 404
; Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
; 547 -----VLYLLIGLV 557
;
; RESULT 6
; US-08-265-428-6
; Sequence 6, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors

```







Best Local Similarity 22.6%; Pred. No. 0.00097;  
Matches 68; Conservative 57; Mismatches 114; Indels 62; Gaps 10;

Qy 164 TDIGWRDLSKFFSDHLEKLPKMDASQAQLLAYKEKHSQSQSQFSDQEIHLHPENV 223  
Db 134 TFVSVSSSSSSKEGSSSYMPSTSSLSAQI-----SSTTRTSTDMKSSSEMIATTV 186  
Qy 224 SALPATVAVASPHHTTSATPKPATLLPTNASVTPSGTSQPOLATTAPPVTTVTSQPPPTLI 283  
Db 187 STTSTSSSTSSSTT--SSTSSSTSSSTSSSTSSSTSSSTSSSTSS--TSS 242  
Qy 284 STVETRAAATLQAMATTAVLT-----TTFOAPTD-----XGSLTI 320  
Db 243 TTSSTSTT--SSTTSIFSVTSSSSSITLSSSEHTTVDSTSPSSTLVPVSSSSTL 299  
Qy 321 PFTISNLTMTG-----NVPNTALSMNVESSTWNTKASWEGREASPGSS 367  
Db 300 STPKVTSMPTSTSTPIVTSVELVTSVVTKAIIVSTDQHOETIFVTRTSVVERSEVAT 359  
Qy 368 SQGSVPENQYGLPEKMLLIGSL-----LFGVLEFLVIGLVLGRILSBSLRKYSRL 420  
Db 360 ATAASNNRNSSTKQRLSGGAIAGIVGVGVIFII--LILLFLIWR---RRKSHDQL 414  
Qy 421 D 421  
Db 415 D 415

RESULT 12  
US-09-294-663-3  
; Sequence 3, Application US/09294663  
; Patent No. 6765127  
; GENERAL INFORMATION:  
; APPLICANT: Granados, Robert R  
; APPLICANT: Wang, Ping  
; TITLE OF INVENTION: A No. 6765127el Invertebrate Intestinal Mucin  
; TITLE OF INVENTION: cdna and Related Products and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Pinnisi & Michaels, P.C.  
; STREET: 118 No. 6765127th Tioga Street  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,663  
; FILING DATE: 19-APR-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/103,429  
; FILING DATE: 24-JUN-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: BTI-39-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (607) 256-2000  
; TELEFAX: (607) 256-3628  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 788 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

Best Local Similarity 22.6%; Pred. No. 0.00097;  
Matches 68; Conservative 57; Mismatches 114; Indels 62; Gaps 10;

Qy 164 TDIGWRDLSKFFSDHLEKLPKMDASQAQLLAYKEKHSQSQSQFSDQEIHLHPENV 223  
Db 134 TFVSVSSSSSSKEGSSSYMPSTSSLSAQI-----SSTTRTSTDMKSSSEMIATTV 186  
Qy 224 SALPATVAVASPHHTTSATPKPATLLPTNASVTPSGTSQPOLATTAPPVTTVTSQPPPTLI 283  
Db 187 STTSTSSSTSSSTT--SSTSSSTSSSTSSSTSSSTSSSTSSSTSS--TSS 242  
Qy 284 STVETRAAATLQAMATTAVLT-----TTFOAPTD-----XGSLTI 320  
Db 243 TTSSTSTT--SSTTSIFSVTSSSSSITLSSSEHTTVDSTSPSSTLVPVSSSSTL 299  
Qy 321 PFTISNLTMTG-----NVPNTALSMNVESSTWNTKASWEGREASPGSS 367  
Db 300 STPKVTSMPTSTSTPIVTSVELVTSVVTKAIIVSTDQHOETIFVTRTSVVERSEVAT 359  
Qy 368 SQGSVPENQYGLPEKMLLIGSL-----LFGVLEFLVIGLVLGRILSBSLRKYSRL 420  
Db 360 ATAASNNRNSSTKQRLSGGAIAGIVGVGVIFII--LILLFLIWR---RRKSHDQL 414  
Qy 421 D 421  
Db 415 D 415

RESULT 12  
US-09-294-663-3  
; Sequence 3, Application US/09294663  
; Patent No. 6765127  
; GENERAL INFORMATION:  
; APPLICANT: Granados, Robert R  
; APPLICANT: Wang, Ping  
; TITLE OF INVENTION: A No. 6765127el Invertebrate Intestinal Mucin  
; TITLE OF INVENTION: cdna and Related Products and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Pinnisi & Michaels, P.C.  
; STREET: 118 No. 6765127th Tioga Street  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,663  
; FILING DATE: 19-APR-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/103,429  
; FILING DATE: 24-JUN-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: BTI-39-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (607) 256-2000  
; TELEFAX: (607) 256-3628  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 788 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

ORIGINAL SOURCE:  
; ORGANISM: Trichoplusia ni  
; TISSUE TYPE: peritrophic membrane  
US-09-294-663-3

Query Match 6.0%; Score 132; DB 4; Length 788;  
Best Local Similarity 31.0%; Pred. No. 0.0021;  
Matches 48; Conservative 15; Mismatches 78; Indels 14; Gaps 6;

Qy 220 PENVSALPATVAVASPHHTTSATPKPATLLPTNASVTPSGTSQPOLATTAPPVTTVTSQPP 279  
Db 96 PAETTOAPAT--TQAPTTQA--PTTTTQAPT--TTTQAPT--TTTQAPT--TTTQAPT 149  
Qy 280 TTLLISTVFTTA--AATLQAMATTAVLT--TTFOAPTD--XGSLTI--PFTISNLTMTG--NVP 338  
Db 150 TQAPTTTQAPT--TTTQAPT--TTTQAPT--TTTQAPT--TTTQAPT--TTTQAPT 208  
Qy 339 TALSMNVESSTWNTKASWEGREASPGSSSQGSVP 373  
Db 209 AATTPAATTPAATPAAT-----TFCVPAPTSAP 237

RESULT 13  
US-09-294-663-4  
; Sequence 4, Application US/09294663  
; Patent No. 6765127  
; GENERAL INFORMATION:  
; APPLICANT: Granados, Robert R  
; APPLICANT: Wang, Ping  
; TITLE OF INVENTION: A No. 6765127el Invertebrate Intestinal Mucin  
; TITLE OF INVENTION: cdna and Related Products and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Pinnisi & Michaels, P.C.  
; STREET: 118 No. 6765127th Tioga Street  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,663  
; FILING DATE: 19-APR-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/103,429  
; FILING DATE: 24-JUN-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: BTI-39-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (607) 256-2000  
; TELEFAX: (607) 256-3628  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 807 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Trichoplusia ni  
; TISSUE TYPE: peritrophic membrane  
US-09-294-663-4

Query Match 6.0%; Score 132; DB 4; Length 807;



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Best Local Similarity 31.0%; Pred. No. 0.0022;
Matches 48; Conservative 15; Mismatches 78; Indels 14; Gaps 6;

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QY 280 TTLLISVFFRA--AATLQAMATTAVLTTFQAPDTSKGSLETIPFTFISNLTNTGNVYNP 338
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QY 339 TALSMNVSSSTWNTKASWEGREASPCSSSQSGVP 373
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RESULT 14
US-08-700-651-12
; Sequence 12, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LRECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4(HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; EARLIER FILING DATE: 1997-08-14
; EARLIER FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12

Query Match 5.8%; Score 129; DB 3; Length 175;
Best Local Similarity 27.3%; Pred. No. 0.00036;
Matches 35; Conservative 15; Mismatches 74; Indels 4; Gaps 1;

QY 226 LPATVAVASPHHTTSATPKPATLLPTNASVTPSGTSQPLATTAPPVTTVTSQPPPTL1ST 285
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QY 286 VFTRAAATLQAMATTAVLTTFQAPDTSKGSLETIPFTFISNLTNTGNVYNPTALSMN 345
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Db 63 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 122
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QY 346 VESSTMNK 353
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Db 123 TTTTITTK 130

RESULT 15
US-08-928-361B-17
; Sequence 17, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA
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; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,361B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,062
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verny, Hana
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-1677
; TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-17

Query Match 5.8%; Score 129; DB 3; Length 175;
Best Local Similarity 27.3%; Pred. No. 0.00036;
Matches 35; Conservative 15; Mismatches 74; Indels 4; Gaps 1;

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QY 286 VFTRAAATLQAMATTAVLTTFQAPDTSKGSLETIPFTFISNLTNTGNVYNPTALSMN 345
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QY 346 VESSTMNK 353
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Db 123 TTTTITTK 130
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Search completed: April 26, 2005, 21:53:37  
Job time : 57 secs

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2	2211	100.0	431	9	US-09-989-723-515	Sequence 515, App
3	2211	100.0	431	9	US-09-989-723-515	Sequence 515, App
4	2211	100.0	431	9	US-09-989-279-515	Sequence 515, App
5	2211	100.0	431	9	US-09-989-727-515	Sequence 515, App
6	2211	100.0	431	9	US-09-944-449-83	Sequence 83, Appl
7	2211	100.0	431	9	US-09-989-731-515	Sequence 515, App
8	2211	100.0	431	9	US-09-944-457-83	Sequence 83, Appl
9	2211	100.0	431	9	US-09-944-862-83	Sequence 83, Appl
10	2211	100.0	431	9	US-09-989-732-515	Sequence 515, App
11	2211	100.0	431	9	US-09-991-073-515	Sequence 515, App
12	2211	100.0	431	9	US-09-945-587-83	Sequence 83, Appl
13	2211	100.0	431	9	US-09-590-442-515	Sequence 515, App

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	121	TDPSLTRLNLPQSOLPOEDSLHQQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD	180
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Qy	181	HLEKLFKXDEASAOQLLAYKEKGHSQSSQFSQDQIEIHLLENVSALPATVAVASPHYTTSA	240
Db	181	HLEKLFKXDEASAOQLLAYKEKGHSQSSQFSQDQIEIHLLENVSALPATVAVASPHYTTSA	240
Qy	241	TPKPTATLLPTNASVTPSGTSOPLATTAPPVTVTSOPPTTLISTVETRAAATLQAMATT	300
Db	241	TPKPTATLLPTNASVTPSGTSOPLATTAPPVTVTSOPPTTLISTVETRAAATLQAMATT	300
Qy	301	AVLTFTFOAPDTSKGSLETIPFTFISNLTNLNTGNVYNPTALSMGNVSSSTNKNKTASWEGR	360
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Qy	421	DYLINGIYVDI 431	
Db	421	DYLINGIYVDI 431	

RESULT 2  
US-09-989-722-515  
; Sequence 515, Application US/09899722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Ban L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC63  
; CURRENT APPLICATION NUMBER: US/09/989,722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
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; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
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; PRIOR FILING DATE: 1998-06-03  
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; PRIOR APPLICATION NUMBER: 60/088876  
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; PRIOR APPLICATION NUMBER: 60/089105  
; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: 60/089440  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089512



APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Nepier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC82  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540

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Db	RESULT 4	
	US-09-989-279-515	
Db	Sequence 515, Application US/09989279	
	Patent No. US20020072496A1	
Db	GENERAL INFORMATION:	
	APPLICANT: Ashkenazi, Avi J.	
Db	APPLICANT: Baker, Kevin P.	
	APPLICANT: Botstein, David	
Db	APPLICANT: Desnoyers, Luc	
	APPLICANT: Eaton, Dan L.	
Db	APPLICANT: Ferrara, Napoleone	
	APPLICANT: Fong, Sherman	
Db	APPLICANT: Gerber, Hanspeter	
	APPLICANT: Gerritsen, Mary E.	
Db	APPLICANT: Goddard, Audrey	
	APPLICANT: Godowski, Paul J.	
Db	APPLICANT: Grimaldi, J. Christopher	
	APPLICANT: Gurney, Austin L.	
Db	APPLICANT: Kljavin, Ivar J.	
	APPLICANT: Napier, Mary A.	
Db	APPLICANT: Pan, James	
	APPLICANT: Paoni, Nicholas F.	
Db	APPLICANT: Roy, Margaret Ann	
	APPLICANT: Stewart, Timothy A.	
Db	APPLICANT: Tamas, Daniel	
	APPLICANT: Watanabe, Colin K.	
Db	APPLICANT: Williams, P. Mickey	
	APPLICANT: Wood, William I.	
Db	APPLICANT: Zhang, Zemin	
	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
Db	TITLE OF INVENTION: Acids Encoding the Same	
	FILE REFERENCE: P27301C56	
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55	PRIOR APPLICATION NUMBER: 60/091778	
56	PRIOR FILING DATE: 1998-07-07	
57	PRIOR APPLICATION NUMBER: 60/091982	
58	PRIOR FILING DATE: 1998-07-07	
59	PRIOR APPLICATION NUMBER: 60/092182	
60	PRIOR FILING DATE: 1998-07-09	

Query Match 100.0%; Score 2211; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.1e-172;  
Matches 431: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 EDCINSCCSTKNTSGDKACNLMIEDTRKTAROPNCYLFFCPNEEACPLKPAKGLMSYRII 120



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QY 241 TPKPATLLPTNASVTPSGTSGQPLATTAPPVTVTSQPPPTLLISTVFTTAAATLQAMATT 300  
Db 241 TPKPATLLPTNASVTPSGTSGQPLATTAPPVTVTSQPPPTLLISTVFTTAAATLQAMATT 300  
QY 301 AVLTTFQAPTDKSGSLETIPETESNLNTGNVNTALSNVSNVESMTMKTASWEGR 360  
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QY 361 EASPGSSSGSPENQYGFPEFKWLLIGSLRCVLFVLVGLVLLGRILSESRRKRYSL 420  
Db 361 EASPGSSSGSPENQYGFPEFKWLLIGSLRCVLFVLVGLVLLGRILSESRRKRYSL 420  
QY 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431

RESULT 5  
US-09-989-727-515  
; Sequence 515, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
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; PRIOR FILING DATE: 1998-03-20  
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Db 361 EASPGSSSQSVPENQYGLPFKWLIGSLFGVLFVIGLVLLGRILSLSLRKRYRSL 420  
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Db 421 DYLINGIYVDI 431

RESULT 6

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; Sequence 83, Application US/09944449  
; Patent No. US20020102647A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,449  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028



APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-06-25  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690

;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;

Best Local Similarity 100.0%; Pred. No. 2.1e-172;

Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFEGGSGSYTLVILICFLTLRLSASQNCCLKSLEDVWIDIOSLSKSGIRGNEPVVTSQ 60  
Qy 61 EDCINSCCSTKNIISGDKACNLMI FDKRTARQPCNYLFCFPNEEACPLKPAKGLMSYRII 120  
Db 61 EDCINSCCSTKNIISGDKACNLMI FDKRTARQPCNYLFCFPNEEACPLKPAKGLMSYRII 120  
Qy 121 TFPSPSLTRNLPSQELPQEDSLHGGQSQAVTPPLAHHTDYSKPTDISWRDITLSQKFGSSD 180  
Db 121 TFPSPSLTRNLPSQELPQEDSLHGGQSQAVTPPLAHHTDYSKPTDISWRDITLSQKFGSSD 180  
Qy 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSSDOETIAHLHPENVVSALPATVAVASPHHTSA 240  
Db 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSSDOETIAHLHPENVVSALPATVAVASPHHTSA 240  
Qy 241 TKPATLLPTNASVTPSGTSQQLATTAPPVTVTVTSQPTTLISTVFTRAAATLQAMATT 300  
Db 241 TKPATLLPTNASVTPSGTSQQLATTAPPVTVTVTSQPTTLISTVFTRAAATLQAMATT 300  
Qy 301 AVLTFTFQAPTSKGSLETPTEISNLTGNTGVNPTALSMNVESSTMNKTASWEGR 360  
Db 301 AVLTFTFQAPTSKGSLETPTEISNLTGNTGVNPTALSMNVESSTMNKTASWEGR 360  
Qy 361 EASPGSSSGSPENQYGLPFKEKWLIGSLLEGLVFLVIGLVGLGRILLESIRRRKYSRL 420  
Db 361 EASPGSSSGSPENQYGLPFKEKWLIGSLLEGLVFLVIGLVGLGRILLESIRRRKYSRL 420  
Qy 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431

RESULT 8

US-09-944-457-83

; Sequence 83, Application US/09944457

; Patent No. US20020110859A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

;; APPLICANT: Botstein, David  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Gerritsen, Mary  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul  
;; APPLICANT: Grimaldi, Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Hillan, Kenneth  
;; APPLICANT: Klijavin, Ivar  
;; APPLICANT: Napier, Mary  
;; APPLICANT: Roy, Margaret  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Wood, William  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P2548P1C1  
;; CURRENT APPLICATION NUMBER: US/09/944,457  
;; PRIOR FILING DATE: 2001-09-26  
;; PRIOR APPLICATION NUMBER: 09/866,028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 60/067,411  
;; PRIOR FILING DATE: December 3, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,334  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,335  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,278  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,425  
;; PRIOR FILING DATE: December 12, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,696  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,694  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,702  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,870  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,873  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/068,017  
;; PRIOR FILING DATE: December 18, 1997  
;; PRIOR APPLICATION NUMBER: 60/070,440  
;; PRIOR FILING DATE: January 5, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,086  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,092  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/075,945  
;; PRIOR FILING DATE: February 25, 1998  
;; PRIOR APPLICATION NUMBER: 60/112,850  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 60/113,296  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 60/146,222  
;; PRIOR FILING DATE: July 28, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: September 16, 1998  
;; PRIOR APPLICATION NUMBER: PCT/US98/25108  
;; PRIOR FILING DATE: December 1, 1998  
;; PRIOR APPLICATION NUMBER: 09/216,021  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 09/218,517  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 09/254,311  
;; PRIOR FILING DATE: March 3, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: September 15, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28409

;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
;; PRIOR FILING DATE: December 1, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: December 16, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: March 2, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: March 30, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: May 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/20710  
;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: February 28, 2001  
;; NUMBER OF SEQ ID NOS: 120  
;; SEQ ID NO 83  
;; LENGTH: 431  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-09-944-457-83

Query Match 100.0% Score 2211; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.1e-172; Indels 0; Gaps 0;  
Matches 431; Conservative 0; Mismatches 0

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Db	61	EDCINSCCSTNNISGDKACNLMIFDTRKTARQPNLCYLFCCNNEACPLKPAKGLMSYRII	120
Qy	121	TDFPSLTNLPSQELPQSDLSLHGQFSOAVTPLAAHHHDYKPTDTSWRDITLSQKFGSSD	180
Db	121	TDFPSLTNLPSQELPQSDLSLHGQFSOAVTPLAAHHHDYKPTDTSWRDITLSQKFGSSD	180
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; Sequence 83, Application US/09944862  
; Patent No. US20020115145A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin

;; APPLICANT: Botstein, David  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Flivaroff, Ellen  
;; APPLICANT: Gerritsen, Mary  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul  
;; APPLICANT: Grimaldi, Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Hillan, Kenneth  
;; APPLICANT: Kijavin, Ivar  
;; APPLICANT: Napier, Mary  
;; APPLICANT: Roy, Margaret  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Wood, William  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P2548P1C1  
;; CURRENT APPLICATION NUMBER: US/09/944,862  
;; CURRENT FILING DATE: 2001-09-26  
;; PRIOR APPLICATION NUMBER: 09/866,028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 60/067,411  
;; PRIOR FILING DATE: December 3, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,334  
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;; PRIOR APPLICATION NUMBER: 60/069,335  
;; PRIOR FILING DATE: December 11, 1997  
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;; PRIOR APPLICATION NUMBER: 60/068,017  
;; PRIOR FILING DATE: December 18, 1997  
;; PRIOR APPLICATION NUMBER: 60/070,440  
;; PRIOR FILING DATE: January 5, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,086  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,092  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/075,945  
;; PRIOR FILING DATE: February 25, 1998  
;; PRIOR APPLICATION NUMBER: 60/112,850  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 60/113,296  
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;; PRIOR APPLICATION NUMBER: 09/216,021  
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;; PRIOR APPLICATION NUMBER: 09/218,517  
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;; PRIOR FILING DATE: March 3, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
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;; PRIOR FILING DATE: No. US200201151451ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. US200201151451ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
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;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
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;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: February 28, 2001  
;; NUMBER OF SEQ ID NOS: 120  
;; SEQ ID NO 83  
;; LENGTH: 431  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-09-944-862-83

Query Match 100.0%; Score 2211; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.1e-172;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MFEGGSLTYTLVILICFLTLRLSASQNCCLKSLEDVVDIQSSLSKGRGNEPVYTSQ 60  
Db 1 MFEGGSLTYTLVILICFLTLRLSASQNCCLKSLEDVVDIQSSLSKGRGNEPVYTSQ 60  
  
QY 61 EDCINSCCTKNIISGDKACNLMIFFDKTKARQPCVLFPCPNEEACPLKPAKGLMSYRII 120  
Db 61 EDCINSCCTKNIISGDKACNLMIFFDKTKARQPCVLFPCPNEEACPLKPAKGLMSYRII 120  
  
QY 121 TDFPSLTRNLPSQELPQEDSLHGFQSVQVTPPLAHHTDYSKPTDISWRDITLSQKFGSSD 180  
Db 121 TDFPSLTRNLPSQELPQEDSLHGFQSVQVTPPLAHHTDYSKPTDISWRDITLSQKFGSSD 180  
  
QY 181 HLEKLFKMDASAQLLAYKEKHSQSSQFSSDQETIAHLHPENVVSALPATVAVASPHTTSA 240  
Db 181 HLEKLFKMDASAQLLAYKEKHSQSSQFSSDQETIAHLHPENVVSALPATVAVASPHTTSA 240  
  
QY 241 TPKPATLLPTNASVTPSGTSQPOLATTPPVTVTSQPTTLISTVFTRAAATLQAMATT 300  
Db 241 TPKPATLLPTNASVTPSGTSQPOLATTPPVTVTSQPTTLISTVFTRAAATLQAMATT 300  
  
QY 301 AVLTITTFQAPTDSKGSLETIPTEISNLTLNTGNVNPPTALSMSNVESSTMNKTASWEGR 360  
Db 301 AVLTITTFQAPTDSKGSLETIPTEISNLTLNTGNVNPPTALSMSNVESSTMNKTASWEGR 360  
  
QY 361 EASPGSSSGSVPEQNYGLPFKWLIIIGSLGVLFLVIGLVLLGRILSESIRRRKYSRL 420  
Db 361 EASPGSSSGSVPEQNYGLPFKWLIIIGSLGVLFLVIGLVLLGRILSESIRRRKYSRL 420  
  
QY 421 DYLLINGIYVDI 431  
Db 421 DYLLINGIYVDI 431

RESULT 10  
US-09-989-732-515  
; Sequence 515, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC57  
;; CURRENT APPLICATION NUMBER: US/09/989,732  
;; CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;

Best Local Similarity 100.0%; Pred. No. 2.1e-172; Indels 0; Gaps 0;  
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Db 181 HLEKLFKMDASAQLLAYKEKGHSQSSQFSQSDQIBIAHLHPENVSAIPATVAVASPHTTSA 240  
Qy 241 TPKPATLLPTNVA SVTPSGTSPQLATTAPPVVTYTSQPTTLISTVTFRAATLQAWATT 300  
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Db 241 TPKPATLLPNASVTSQTSQPOLATAPVTTVTSQPTTLISTVFTRAAATLQAMATT 300  
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Qy 361 EASPGSSSGSVENQYGLPFKWLIGSLFCGLVFLVGLVGLILSESILRRKYSRL 420  
Db 361 EASPGSSSGSVENQYGLPFKWLIGSLFCGLVFLVGLVGLILSESILRRKYSRL 420  
Qy 421 DYLINGIYVDI 431  
Db 421 DYLINGIYVDI 431

RESULT 11  
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; Sequence 515, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
; CURRENT APPLICATION NUMBER: US/09/991,073  
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Query Match 100.0%; Score 2211; DB 9; Length 431;

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RESULT 12

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; Patent No. US20020127643A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548F1C1  
; CURRENT APPLICATION NUMBER: US/09/945,587  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
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; PRIOR APPLICATION NUMBER: 60/069,425

Query Match 100.0%; Score 2211; DB 9; Length 431;

## RESULT 1.3

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmitted
; FILE OF INVENTION: Acids Encoding
; FILE REFERENCE: P27301C8
; CURRENT APPLICATION NUMBER: US/09/990442
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-06-16

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[illegible]

;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.1e-172;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFPGGSLTYLVIIICFLTLRLSASQNCCLKSLEDVWIDIOSLSKGIKRGNEPVYTSTQ 60  
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1 MFPGGSLTYLVIIICFLTLRLSASQNCCLKSLEDVWIDIOSLSKGIKRGNEPVYTSTQ 60  
Qy 61 EDCINSCCTKNISGDKACNLMI FDKRTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 EDCINSCCTKNISGDKACNLMI FDKRTARQPCNYLFFCPNEEACPLKPAKGLMSYRII 120  
Qy 121 TDFPSLTRNLPSQELPQEDSLHGHQFSQAVTPLAHHTDYSKPTDISMRDITLSQKFGSSD 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 TDFPSLTRNLPSQELPQEDSLHGHQFSQAVTPLAHHTDYSKPTDISMRDITLSQKFGSSD 180  
Qy 181 HLEKLFQMDASAQLLAYKEKHSQSSQFSQSSQOETIAHLIPENVSALPATVAVASPHTTSA 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 HLEKLFQMDASAQLLAYKEKHSQSSQFSQSSQOETIAHLIPENVSALPATVAVASPHTTSA 240  
Qy 241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLITSTVETRAAATLQAMATT 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 TPKPATLLPTNASVTPSGTSQPOLATTAPPVTVTSQPTTLITSTVETRAAATLQAMATT 300  
Qy 301 AVLTITTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSNSVSESMTNKKTASWEGR 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 AVLTITTFQAPTDSKGSLETIPTEISNLTNTGNVYNPTALSNSVSESMTNKKTASWEGR 360  
Qy 361 EASPGSSQGVSPENQYGLPFFKWLIGSLLFGVLFLVIGLVLGRILSESILRRKYSRL 420  
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361 EASPGSSQGVSPENQYGLPFFKWLIGSLLFGVLFLVIGLVLGRILSESILRRKYSRL 420  
Qy 421 DYLINGIYVDI 431  
Db |||||||||||  
421 DYLINGIYVDI 431

RESULT 14  
US-09-991-163-515  
; Sequence 515, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C17  
;; CURRENT APPLICATION NUMBER: US/09/991,163  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
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;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
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; PRIOR APPLICATION NUMBER: 60/091633  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2211; DB 9; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2,1e-172;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MFCGEGSLVTVIIICFLTLRLSASONCLKKSLEDVVIIQSSLSKIRGNEPVYTSQ	60
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Db	61	EDCINSCCSTKNISGDKACNLMIFDTRKTARQPCNYLFFCPNEACPLKPAKGLMSYRII	120
Qy	121	TDFPSLTRNLPSQBELPOEDSLHQCFSQAVTPLAHHTDYKPTDISWRDTLSOKFGSSD	180
Db	121	TDFPSLTRNLPSQBELPOEDSLHQCFSQAVTPLAHHTDYKPTDISWRDTLSOKFGSSD	180
Qy	181	HLEKLFYKDEASAOQLLAYKEKGHSQSSQFSDQSIHLLPENVSALPATVAVASPHTTSA	240
Db	181	HLEKLFYKDEASAOQLLAYKEKGHSQSSQFSDQSIHLLPENVSALPATVAVASPHTTSA	240
Qy	241	TPKPATLLPTNASVTPSGTSQPLATTAPPVTVTSQPTTLISTVFTRAAATLQAMATT	300
Db	241	TPKPATLLPTNASVTPSGTSQPLATTAPPVTVTSQPTTLISTVFTRAAATLQAMATT	300
Qy	301	AVLTTFQAPTDGSGSLETIETFEISNLTLNTGNVNTALSMNSVESTWTKTASWGR	360
Db	301	AVLTTFQAPTDGSGSLETIETFEISNLTLNTGNVNTALSMNSVESTWTKTASWGR	360
Qy	361	EASPGSSSQSVPENQVGLPPEKWLIIIGSLIFGLVFLVIGLVLGRILSESILRRKYSRL	420
Db	361	EASPGSSSQSVPENQVGLPPEKWLIIIGSLIFGLVFLVIGLVLGRILSESILRRKYSRL	420

QY 421 DYLINGIYVDI 431  
 Db 421 DYLINGIYVDI 431

## RESULT 15

US-09-945-015-83

; Sequence 83, Application US/09945015  
 ; Patent No. US20020132768A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fierro, Ellen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1  
 ; CURRENT APPLICATION NUMBER: US/09/945,015

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222

; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330

; PRIOR FILING DATE: September 16, 1998

; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
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 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-09-945-015-83

Query Match 100.0%; Score 2211; DB 9; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-172;  
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFGEGSLTYTLVLIICFLTLRLSASQNCLEKSLSDVVIDIQSSLSKGRGNEPVYTSTQ 60  
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 QY 361 BASPGSSQSGVPENQYGLPFKEKMLLIGSLFGVLFLVIGLVLLGRILSESRLRRKYSRL 420  
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Qy 421 DYLINGIYVDI 431  
| | | | | | | | | |  
Db 421 DYLINGIYVDI 431

Search completed: April 26, 2005, 22:25:34  
Job time : 1467 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2005, 21:38:57 ; Search time 52 Seconds  
(without alignments)  
797.489 Million cell updates/sec

Title: US-10-735-014-83  
Perfect score: 2211  
Sequence: 1 MFPGEGSLTYTLVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	174.5	7.9	825	T29634	hypothetical prote
2	160.5	7.3	477	S53362	mucin 5AC (clone J
3	155.5	7.0	770	T22808	hypothetical prote
4	154.5	7.0	851	T22696	hypothetical prote
5	154	7.0	534	T39903	serine-rich protei
6	151.5	6.9	1251	T21389	hypothetical prote
7	150.5	6.8	797	VGBEX1	glycoprotein X pre
8	150.5	6.8	860	JC4566	chitinase (EC 3.2.
9	149.5	6.8	3020	A43932	mucin 2 precursor,
10	149.5	6.8	3570	T45025	mucin MUC5B, trach
11	147.5	6.7	790	T34293	hypothetical prote
12	147.5	6.7	1609	S25345	probable membrane
13	147	6.6	662	A45155	mucin FIM-C.1 - Af
14	146	6.6	786	A47547	serine proteinase
15	144.5	6.5	505	B46629	mucin 6, gastric (
16	144.5	6.5	1104	S59310	probable membrane
17	143	6.5	626	S53871	Pmel 17 protein -
18	142.5	6.4	377	A48018	mucin 7 precursor,
19	142.5	6.4	491	A49179	melanoma antigen h
20	142.5	6.4	866	T45462	membrane glycoprot
21	142.5	6.4	867	T45463	membrane glycoprot
22	141.5	6.4	1161	S57180	probable membrane
23	141	6.4	1777	T34369	hypothetical prote
24	140	6.3	292	S24169	mucin - rat
25	140	6.3	1275	T33369	hypothetical prote
26	138	6.2	909	ORX112	LDL receptor 2 pre
27	137.5	6.2	1630	A53577	ascites stialoglyco
28	137	6.2	528	T47141	gastric mucin (clo
29	136.5	6.2	1229	T25697	hypothetical prote

30	136	6.2	503	2	S63257	probable membrane
31	136	6.2	796	2	T21460	hypothetical prote
32	135.5	6.1	322	2	A53715	apomucin precursor
33	135.5	6.1	543	2	S35047	mucin JUL7 - human
34	135.5	6.1	1299	2	T47182	hypothetical prote
35	135.5	6.1	2271	2	F90073	hypothetical prote
36	134	6.1	164	2	I53641	mucin 5AC - human
37	133.5	6.0	708	2	T19474	hypothetical prote
38	133.5	6.0	3507	2	T34513	hypothetical prote
39	133	6.0	556	2	S31892	probable membrane
40	133	6.0	610	2	S35049	mucin JER57 - huma
41	133	6.0	636	2	S63131	probable membrane
42	133	6.0	1075	2	S48992	floculation prote
43	133	6.0	1367	2	S51959	hypothetical prote
44	132	6.0	1162	2	JH0557	exo-alpha-sialidas
45	131	5.9	725	2	A41258	a-agglutinin core

ALIGNMENTS

RESULT 1

T29634  
hypothetical protein C12D12.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29634  
R:Nhan, M.; Hawkins, J.  
submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid C12D12.  
A:Reference number: Z20656  
A:Accession: T29634  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-825 <NHA>  
A:Cross-references: UNIPROT:Q17921; EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP: C12D12  
A:Experimental source: strain Bristol N2; clone C12D12  
C:Genetics:  
A:Gene: CESP:C12D12.1  
A:Map position: X  
A:Introns: 48/1, 86/3; 137/1, 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1  
C:Superfamily: Epstein-Barr virus membrane antigen gp350

Query Match 7.9%; Score 174.5; DB 2; Length 825;  
Best Local Similarity 23.7%; Pred. No. 0.00064;  
Matches 93; Conservative 40; Mismatches 144; Indels 115; Gaps 17;

QY	52	NEPVYTSQED-----CINSCCSTKNISGDKACNLMIPDTRK-----	88
DB	363	NTPFTRNANDTIEIYCTVLSCSITIDGVK---IQITDKVQVKVDDISYIFVNTIAN	419
QY	89	-----TARQPCNYLFFC-----PNEEACPLKP--AKGLMSY---RIITDF	123
DB	420	PGYHOISUKQGSYAFFYGNKNLYSYGEGGANKPTVVLPAPPTPGPTFYPTVVTSTWS	479
QY	124	PSLTNLNPSQELPQSDLSLLHGQFSQAVTPLAAHHHDYSKPTDISWRDITLSQKFGSSDHLE	183
DB	480	PPTTVTVPTTTPFP-----TTNTTPPANPTT--ATPTTVG---TSKQNTNISPHLS	526
QY	184	KLFQWDEASQAQLLAYKEG-----HSQSQFSSDQEIHAHLLENVSALPATVAVASPH	236
DB	527	TTTGSIVTSTPTMAPQTSASPTTTHHTTASQPTTKPV--VTNNSVTPSTGTTTVPVP-	583
QY	237	TTSATPKPATLLPTNASVTPGSTQPOLATTAPPVTTVTSQPTTLISVTFVRAAATLOA	296
DB	584	TTTGSTTQTQTAPVTKPTVPSSTTQ-----TAPPVTTPTSPQPPVTTSLTTLTTPTPVP	638
QY	297	MAT-----TAVLTITFOA-----PTDSKGSLEITPPT	323
DB	639	TTTVVPSSATVPTTPTTVAATTTSKAPVVTTTSPTLAPTSPTKLPTSPSPSTVGTSP-T	697
QY	324	EISNLTNLNGVNYNPNTALSMGNVESTWNKTA	355

Db 698 APANLTPTTAPVNPVT--SSTTAPVNPPTS 727

RESULT 2

S53362

mucin SAC (clone JER47) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Oct-1996 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004

C;Accession: S53362; S71065

R;Guyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galiegue-Biochem. J. 305, 211-219, 1995

A;Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich domain

A;Reference number: S53361; MUID:95126907; PMID:7826332

A;Accession: S53362

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-477 <GUY>

A;Cross-references: UNIPROT:Q14887; EMBL:Z34277

A;Experimental source: clone JER47

R;Porchet, N.

submitted to the EMBL Data Library, June 1994

A;Reference number: S71065

A;Accession: S71065

A;Molecule type: mRNA

A;Residues: 1-211, 'S', 213-224, 'AR', 227-259, 'S', 261-477 <POR>

A;Cross-references: EMBL:Z34277; NID:9563374; PIDN:CAA84031.1; PID:9563375

A;Experimental source: clone JER47

C;Genetics:

A;Gene: GDB:MUC5AC

A;Cross-references: GDB:454136; OMIM:158373

A;Map position: lip15.5-lip15.5

C;Keywords: glycoprotein; tandem repeat

Query Match 7.3%; Score 160.5; DB 2; Length 477;

Best Local Similarity 23.8%; Pred. No. 0.0028;

Matches 76; Conservative 41; Mismatches 117; Indels 85; Gaps 13;

Qy 147 SQAVTPLAHHTDYKPTDISW-----RDTLSQKFGSSDHL-----EKLFRMD--- 189

Db 15 SQVTRDCHLCTWKFVDVDFPSPGGGKQYNNIRSGEKICRRPEITLQCRAE 74

Qy 190 ---EASAQLLAY-----KEKG-----HSQSQFSS---DOEIAHLLPENVSALPATVAVAS 234

Db 75 SHPEVSIHLQVQVCSREGLVCRNQDQGFPMCLNVEVRVLCCEPKGCPVT---ST 131

Qy 235 PHTTSATPKPATLPTNAS-----VTPSGTSOPOLATTAPPVTTVSQPTTLI 283

Db 132 PVTAPSTPSGRATSPQSTSSWQKSRITLVTITSTPQTSITTSAPTSTTSAPTSTT 191

Qy 284 STVETRAAATLQAMATTAVLTTFQAPDTSKGSLET-----IPFTISNLT 330

Db 192 SAPTTSTSTPQTSISSAPTSTTSAPTSTTSAPTSTTSAPTSTTSAPTSTTSAT- 250

Qy 331 NTGNVYNPTALSMGNE-----SSTMNKTASWEGREASP-----GSSSQGSVPEN 375

Db 251 TTSITSAPTTSTSPQSKTSAASTSSGTTSPSPVTTTSTASVSKTSTSHVSVSKT 310

Qy 376 QYGLP-----FEKW 384

Db 311 THSQVTRDCHPCTWTWK 329

RESULT 3

T22808

hypothetical protein F56H9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T22808

R;Burton, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19618

A;Accession: T22808

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-770 <WIL>

A;Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5

A;Experimental source: clone F56H9

C;Genetics:

A;Gene: CESP:F56H9.1

A;Map position: 5

A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Query Match 7.0%; Score 155.5; DB 2; Length 770;

Best Local Similarity 32.7%; Pred. No. 0.011;

Matches 48; Conservative 16; Mismatches 64; Indels 19; Gaps 5;

Qy 219 LPENVSALPATVAVASPHHTTSATPKPATLPTNASVT-----PSGTSQPOLATTAPPV-- 271

Db 93 VPPTTSTTTTIV--PPITTSITTTTVPPTTSSITTTTVPPTTSSITTTTVPPTT 150

Qy 272 --TTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAPDTSKGSLETIPFTISNLT 329

Db 151 TSTTTTVPPTTSTTTTTPAT-----TTSTATTTTVPPTTSTTTTVPPTTSTTTT 205

Qy 330 LNTGNVYNPTALSMNVESSTMNKTAS 356

Db 206 TTT---VPPTTSSITTTTTPPTT 229

RESULT 4

T22696

hypothetical protein F55B11.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T22696

R;Ainscough, R.

submitted to the EMBL Data Library, December 1996

A;Reference number: Z19601

A;Accession: T22696

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-851 <WIL>

A;Cross-references: UNIPROT:O17893; EMBL:Z83318; PIDN:CAB05903.1; GSPDB:GN00022; CESP:F5

A;Experimental source: clone F55B11

C;Genetics:

A;Gene: CESP:F55B11.3

A;Map position: 4

A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3

Query Match 7.0%; Score 154.5; DB 2; Length 851;

Best Local Similarity 26.6%; Pred. No. 0.014;

Matches 47; Conservative 26; Mismatches 89; Indels 15; Gaps 4;

Qy 219 LPENVSALPATVAVAS-----PHTTSATPKPATLPTNASVTPSGTSQPOLATTAPPVT 272

Db 377 VPPTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTT 436

Qy 273 TTVTSQPPTTLISTVFTRAAATLQAMA--TTAVLTTFQAPDTS---KGSLETIPFTIS- 326

Db 437 TTVTPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTT 496

Qy 327 ---NLTLNTGNVYNPTALSMNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLP 380

Db 497 PTTTTPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTTSTTTTVPPTT 553

RESULT 5

T39903

serine-rich protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T39903

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, November 1998

A;Reference number: Z21889

A;Accession: T39903

Db 142 DGKQTNLRNGGCCSETSIQVLNSSDS--TWIIITLTSOSWKNKANALINLLYCTPN--ACP 191  
 Qy 108 LKPAKGLMSYRIIITDFPSLT-----RNLPSEQBELPOEDSLHGHQFQAVTFLAHHHTDYSPK 163  
 Db 198 QOSMLWTNCSNLSTTSSSTWLSSTLLTTETETRESSTGS-IQTTPTPSTEPSITITTP 256  
 Qy 164 TDISWRDTLSQKFGSSDHLEKLFKMDERASAOQLLAYKEKGHSQSQSFSSDQEIHAHLLPENV 223  
 Db 257 ME-----QSSSTVSS----- 265  
 Qy 224 SALPATVAVASPHHTTSATPKPATLLPTNASVTPSGTSQOPALATAPPVTVTSQBPPTLLI 283  
 Db 266 -----VOKRTYSEDKPPSSSTVTPISASTSEGSTSP-MAETSSSSSTTQSSSPAST-- 314  
 Qy 284 STVFTRAAATLQAMATTAV--LTTTFQAPTDSKGSLETIPTEISNLTLNTGNVNPATL 341  
 Db 315 STV--PSSIVGSPPTGLTTLSTNEQSTSSSGHSTSTGTGTYSE-TPEISTDFTAST 371  
 Qy 342 S-----MSNVESSTWNKVTASWEGREASPGSSSQGSVPENQYGLPF--EKWLL 386  
 Db 372 SSSSDSTQSSNAQSTIENGSTTTNFTSAPSTSSPATPTTYNNWPCTGTTWML 426  
  
 RESULT 7  
 VBEX1  
 glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p)  
 C:Species: equine herpesvirus 1  
 A:Note: host Equus caballus (domestic horse)  
 C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C:Accession: H36802  
 R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
 submitted to GenBank, March 1992  
 A:Description: The DNA sequence of equine herpesvirus-1.  
 A:Reference number: A36805  
 A:Accession: H36802  
 A:Molecule type: DNA  
 A:Residues: 1-797 <TEL>  
 A:Cross-references: UNIPROT:P28968; GB:M66664; NID:G330791; PIDN:AAB02506.1; P:  
 R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
 Virology 189, 304-316, 1992  
 A:Title: The DNA sequence of equine herpesvirus-1.  
 A:Reference number: A41831; MUID:92295566; PMID:1318606  
 A:Contents: annotation; possible protein-coding frames  
 A:Note: neither amino acid nor nucleotide sequence is given  
 C:Genetics:  
 A:Gene: 71  
 C:Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycopro  
 C:Keywords: Glycoprotein; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <Sig>  
 F:23-797/Product: glycoprotein X #status predicted <Mat>  
 F:23-465/Region: serine/threonine-rich  
 F:489-797/Domain: equine herpesvirus 1 glycoprotein homology <EHG>  
 F:766-790/Domain: transmembrane #status predicted <TMN>  
 F:590/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
 Query Match 6.8%; Score 150.5; DB 1; Length 797;  
 Best Local Similarity 24.3%; Pred. No. 0.025;  
 Matches 58; Conservative  
  
 Qy 158 TDYSKPTDISWRDTLSQKFGSDHLEKLFKMDERASAOQLLAYKEKGHSQSQSFSSDQEIHA 217  
 Db 29 TTSSSTSGSGQSTSSGTTNSSSSPPTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSS 88  
 Qy 218 LLENVSALPATVAVASPHHTTSATPKPATLLPTNASVTP----- 256  
 Db 89 SAPSTASSSTSIPTSTSTETTTTPTASTTTPTTTTAAPTTAATTAVTTAASTSAETTT 148  
 Qy 257 ---SGTSQPOLAT-TAPPVTVTSQBPPTLLISTVFTRAAATLQAMATTAVLTTFQAPTD 312  
 Db 149 ATATASTPTTPTSTTTTATTTVPTTASTTDTTAAATTAATTAATTAATTAATTA 208  
 Qy 313 SKGSLETIPTEISNLTLNTGNVNPATLSMNSVNPSTMTKNTASWEGREASPGSSSQGS 371



QY 276 SQPPTLLIS-----TVFTRAAATLQAMATTAVLTTFQAPDTSKGSLETIPPT 323  
Db 1571 TPEPTTPSPPTTTPSPPTTITTTTPPTTPSPPTT---TTTPPTTPSPPTTPTIT 1627  
QY 324 EISNLT 329  
Db 1628 PPTSTT 1633  
RESULT 10  
T45025  
mucin MUC5B, tracheobronchial [imported] - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45025  
R:Desseyn, J.L.; Guyonnet-Duperrat, V.; Porchet, N.; Aubert, J.P.; Laine, A.  
J. Biol. Chem. 272, 3168-3178, 1997  
A:Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat  
A:Reference number: 222899; MUID:97166151; PMID:9013550  
A:Accession: T45025  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-3570 <DES>  
A:Cross-references: EMBL:272496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503  
A:Experimental source: placenta  
C:Genetics:  
A:Gene: MUC5B  
Query Match 6.8%; Score 149.5; DB 2; Length 3570;  
Best Local Similarity 30.5%; Pred. No. 0.19; Mismatches 58; Indels 61; Gaps 10;  
Matches 62; Conservative 22; Mismatches 58; Indels 61; Gaps 10;  
QY 204 SSSQSSQEIHAHLLPENVSALPATVAVA-SPHTTSATPKPATLLPTNASVTPSGTSQP 262  
Db 626 SKATPSS-----PGTATAPALRSTATPTATSPAISSSI-----GTTWT 568  
QY 263 QIATATPPTTV-----TSQPPTLLISTVFTRAAATLQAMA-----TTAVLT 304  
Db 669 RLSQITTPMATSTAPSSPTPETVHTSTVLTITATTGTATGVSATPSTPGTAHTTKVLT 728  
QY 305 TT---FQA-PTDSKGSLETIPTEISNLTNT-----GNVNPATLSMNVES 348  
Db 729 TTTTGTATPSSPGARTLP-WIISTTTPTTRGTVTPSSIPGTHPTVLTITTTTV 787  
QY 349 STMNKTASWEGREASPGSSSQS 371  
Db 788 AT-----GSMATPSSSTQTS 802  
RESULT 11  
T34293  
hypothetical protein F49E10.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T34293  
R:Miller, N.  
submitted to the EMBL Data Library, April 1996  
A:Description: The sequence of C. elegans cosmid F49E10.  
A:Reference number: 221500  
A:Accession: T34293  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-790 <MIL>  
A:Cross-references: UNIPROT:Q20539; EMBL:U53341; PIDN:AAC69106.1; GSPDB:GN000028; CESP:F4  
A:Experimental source: strain Bristol N2; clone F49E10  
C:Genetics:  
A:Gene: CESP:F49E10.2  
A:Map position: X  
A:introns: 51/1; 92/3; 176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1; 732/3  
Query Match 6.7%; Score 147.5; DB 2; Length 790;  
Best Local Similarity 25.6%; Pred. No. 0.039;  
Matches 60; Conservative 34; Mismatches 107; Indels 33; Gaps 11;

QY 152 PLAAHHTDYSKPTDISWRDTLSQKF--GSSDH--LEKLFKMDASQAQLLAYKEKHSQSS 207  
Db 537 PGFHNRRFSK-KDLG----LPEGFVGQSQVRIEK--KQGFATLPLRKVSTVPPTTST 589  
QY 208 QFSSDQEIHAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPLATT 267  
Db 590 SSTTQK-----PSTTTVPSTPTSTTTTTTPKPTTSTSTSTSTSTTTTTTTTATT 644  
QY 268 APPVTTVTSQPPTLLISTVFTRAAATLQAMATTAVLTTFQA-----PTDSKGSLETIPF 322  
Db 645 PPTTTTITSEKPVLTITQTWTAPPTTVKRTPTQVTPTKIPRWPLAGSGSTEQ-PW 703  
QY 323 TESISNLTNTGNVNPATLSMNVESSTWNKTASWEGREASPGSSSQSGSVPENQ 376  
Db 704 WQ-----KVQTGQNTLPLPLFPVSKRVEEKVKS-----AKP-NESDNKIPEQK 746  
RESULT 12  
S25345  
probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YCR1102  
C:Species: Saccharomyces cerevisiae  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: S25345; S19504  
R:Wilson, C.; Grisanti, P.; Frontali, L.  
Yeast 8, 569-575, 1992  
A:Title: The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromo  
A:Reference number: S25345; MUID:92397594; PMID:1523889  
A:Accession: S25345  
A:Molecule type: DNA  
A:Residues: 1-1609 <WIL>  
A:Cross-references: UNIPROT:P25653; GB:X59720; EMBL:S43845; NID:g1907116; PIDN:CAA42254  
R:Frontali, L.; Grisanti, P.  
submitted to the Protein Sequence Database, March 1992  
A:Reference number: S19504  
A:Accession: S19504  
A:Molecule type: DNA  
A:Residues: 1-1609 <FRO>  
A:Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227; MIPS:YCR089w  
A:Gene: SGD:PIG2  
A:Cross-references: SGD:S0000685; MIPS:YCR089w  
A:Map position: 3R  
C:Keywords: transmembrane protein  
F:4-20/Domain: transmembrane #status predicted <TM1>  
F:1592-1609/Domain: transmembrane #status predicted <TM2>  
Query Match 6.7%; Score 147.5; DB 2; Length 1609;  
Best Local Similarity 22.4%; Pred. No. 0.095;  
Matches 88; Conservative 63; Mismatches 164; Indels 77; Gaps 14;  
QY 41 IOSSLKSGIRGNEPVYVTSQEDCINSCCTKINISGDKACNLMIFDTR-----KTARQPNY 96  
Db 1057 IMSSSNVISTNEKPSSTTSPYNSGYSLPSSSTPSQYSLSTATTINGIKTV-----Y 1111  
QY 97 LFFCPNEEACPLKPAKGLMSYRIITDFPSLTNLPSQELPOEDSLHGFQSVATVPLAH 156  
Db 1112 TWCPLAEKSTV--AASSQSSRSVDRFVSSSK--PSSLSQ--TSQYTLSTATTISGL 1165  
QY 157 HTDYSKPTDISWRDTLSQKFSSDHLE-KLFKMDASQAQLLAYKEKHSQSSQ-----F 209  
Db 1166 KTVYTTWCPLTSKSTLGATQTSSTAKVITSSASSATSSISLSTSESSSGYLSKV 1225  
QY 210 SSDQEIHAHLLPENVSALPATVAVAGP-----HTTSATPKPAT-----LLPTNASV 254  
Db 1226 CSGTECTQDVPTQ-SSSPASTLAYSPSVSTSSSSSFSTTASTLTSTHTSVPLPSSSI 1284  
QY 255 TSGTSGSQPLATT---APVTTVTQPPPTLLISTVFTRAAATLQAMA-----TTAVLT 304  
Db 1285 SASSPSSSTLLSTSLFSPAFSTSTLPTATAVSSSTFIASSLPLSSKSLSPVSSILM 1344  
QY 305 TTFQAPTDSKGSLETIPTEISNLTNTGNVNP----- 339

```
Db 1345 SQFSSSSSSSLASLPSLSISP-TVDTVSLQPTTGIATLTCTDSQQQEVSTICNGSN 1403
Qy 340 ---ALSMNVESSTMNTKASWEGREASPGSSS 368
Db 1404 CDDVTSTATTPTSTVTDITCTGSECOKTTSS 1435

RESULT 13
mucin FIM-C.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45155
P;Hauser, F.; Hoffmann, W. 24624, 1992
J. Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cytosine-rich modules in integrin mucin C.1 (FIM-C.1)
A;Reference numbers: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
F;162-202/Domain: trefoil homology <TRF1>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>

Query Match 6.6%; Score 147; DB 2; Length 662;
Best Local Similarity 26.9%; Pred. No. 0.033;
Matches 49; Conservative 19; Mismatches 78; Indels 36; Gaps 5;

Qy 228 ATVAVASHTTSAPKPAALLPTNASVTPSGTSQPQLATAPPVTT-----VTSQPP 279
Db 394 STSQVAATKTT--TPTTTTTTTTTTTTAKATTTTPTTTTTTTTTTTTTTTTAKATTTPT 451

Qy 280 TLLSTVFTRAAATLQAMATTAVLTTFQAPDTSKGSLETIPTEISNLTNTGNYNPT 339
Db 452 TTTPTTTTTTAKATTTPTTTTTTTTTTTTAKATTTTPTTTTTTTTTTTTAKATTTT-----PT 506

Qy 340 ALSMNVESSTMNTKAS-----WEGREASPGSSSQGSVPENQ----YG 378
Db 507 TTTTITTTTAKATTTTTSCEKRWPSKRADCGVPGITESQCHSKGCCPDSSIPQTKWCFYS 566

Qy 379 LP 380
Db 567 LP 568

RESULT 14
A47547
serine proteinase stubble-stubloid (EC 3.4.21.-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A47547
R;Appel, L.F.; Prout, M.; Abu-Shumays, R.; Hammonds, A.; Garbe, J.C.; Fristrom, D.; Fristrom, D.; Acad. Sci. U.S.A. 90, 4937-4941, 1993
A;Title: The Drosophila stubble-stubloid gene encodes an apparent transmembrane serine
A;Reference number: A47547; MUID:93281671; PMID:7685111
A;Accession: A47547
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-786 <APP>
A;Cross-references: UNIPROT:Q05319; GB:L11451; NID:g158511; PIDN:AAA28918.1; PID:g158512
C;Genetics:
A;Gene: Sb-sbd
A;Cross-references: FlyBase:FBgn000319
C;Superfamily: serine proteinase stubble-stubloid; trypsin homology
C;Keywords: hydrolase; serine proteinase; transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TMN>
F;543-781/Domain: trypsin homology <TRY>
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Query Match 6.6%; Score 146; DB 1; Length 786;
Best Local Similarity 21.0%; Pred. No. 0.048;
Matches 74; Conservative 47; Mismatches 162; Indels 70; Gaps 9;

Qy 63 CINS----CCSTKNI SGDKACNLMI FDRKTRKARQPCNYLFFCNEEACPLKPAKGLMSYR 118
Db 164 CVDSEFMFGSCCTHNYTD---NIVLPQTAFSYTRPTKPLTLRPRPPAAPYKP----- 211

Qy 119 IITDFSLRNLPSELPOEDSLLHGQFSQAVTPLAHHHTD-----YSKPTDISW 168
Db 212 -----MISGMTIERP-----HGAGTVIRPSPGHGQTLARPHPPYQSKPT----- 254

Qy 169 RDTLSQKFGSSDHLKFLKMDKASQAQLLAYKKGHSQSSQFSQDQELAHLLPENVSAL-- 226
Db 255 --TASDLHGASHPSSSSSSSSSSSNPNFSIWHSTTQQQQQHQHQNHQWMTPEFSITK 312

Qy 227 -----PATVAVASPHTTSS-----ATPKPATLLPTNASVTPSGTSQPQLA 265
Db 313 PRPTGWTKPGIVNLPMPARPSKPSKTKPKIVYDRSPPPSPSPSTSTSTSTSLIWPA 372

Qy 266 TTAPPVTTVTSQPTTILSTVFTRAATLQAMATTAVLTTFQAPDTSKGSLETIPTEI 325
Db 373 QTHPPQPHRPTRPQLSGTSLAASSSSSHWPSSTTSTSTSTSTTTTTTTTTTTTTTTT 432

Qy 326 SNLTLN--TGNVYNPTALSMNVESSTMNTKASWEGREASPGSSSQGSVPENQ 376
Db 433 RRTTNKPTRPYQPTTATSSSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 485

RESULT 15
B46629
mucin 6, gastric (3-repeat clone) - human (fragment)
N;Alternate names: MUC6
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46629
J;Toribara, N.W.; Robertson, A.M.; Ho, S.B.; Kuo, W.L.; Gum, E.; Hicks, J.W.; Gum Jr., J.
R. Biol. Chem. 268, 5879-5885, 1993
A;Title: Human gastric mucin. Identification of a unique species by expression cloning.
A;Reference number: A46629; MUID:93194895; PMID:7680650
A;Accession: B46629
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-505 <TOR>
A;Cross-references: UNIPROT:Q14395; GB:L07518; NID:g292045; PIDN:AA561945.1; PID:g292046
A;Experimental source: stomach
A;Note: sequence extracted from NCBI backbone (NCBIN:128397, NCBI:128399)
C;Genetics:
A;Gene: GDB:MUC6
A;Cross-references: GDB:134734; OMIM:158374
A;Map position: 11p15.5-11p15.5
C;Keywords: glycoprotein
```

```
Query Match 6.5%; Score 144.5; DB 2; Length 505;
Best Local Similarity 23.9%; Pred. No. 0.035;
Matches 78; Conservative 37; Mismatches 101; Indels 111; Gaps 15;

Qy 89 TARQPCNYLFFCNEEACPLKPAKGLMSYRIITDFPSLRNLPSELPOEDSLAH-QQFS 147
Db 116 SSRPPPPPTTHSPPTGSSPFS-STGPMT---ATSFKT-TTTPPTPSLPQTPLTHVPPFS 170

Qy 148 QA-VTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLKFLKMDKASQAQLLAYKKGHSQS 206
Db 171 TSLVTPITH--TVITPT-----HPQ- 188

Qy 207 SQFSSDQELAHLLPENVSALPATV-----AVASPHTTSTATPKATLLP 249
Db 189 ---MSTSAIYHSTPTGTIASPTTVKATRTVTAPLMTATTSRISQAHSSISTAKTSLH 245

Qy 250 TNAS-----VTPSGTSQQLATTAPPVTTV-----SQPTTLLS-----TVF 287
Db 246 SHASSTHHEVPTSTTNVTPKSTSR-----DTSPVTHHTTSATSSRRPTPTTHSSPTRS 301
```



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2005, 20:26:45 ; Search time 122 Seconds  
(without alignments)  
1809.067 Million cell updates/sec

Title: US-10-735-014-83

Perfect score: 2211

Sequence: 1 MFFGEGSLTYTLVLCFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	2211	100.0	431	1	MNS1_HUMAN	Q9H8J5 homo sapien
2	2039	92.2	431	1	MNS1_MACFA	Q9SKG7 macaca fasc
3	2022	91.5	397	2	Q9NW60	Q9NW60 homo sapien
4	1164.5	52.7	414	1	MNS1_MOUSE	Q9ct33 mus musculus
5	503	22.7	194	2	Q8X0I0	Q8X0I0 mus musculus
6	197.5	8.9	392	2	Q8VCP2	Q8VCP2 mus musculus
7	197	8.9	449	2	Q9H2K4	Q9H2K4 homo sapien
8	196.5	8.9	392	2	Q9D8N1	Q9D8N1 mus musculus
9	188	8.5	449	2	Q96F05	Q96F05 homo sapien
10	180.5	8.2	1349	2	Q8WQ04	Q8WQ04 homo sapien
11	168	7.6	519	2	Q7YTR7	Q7YTR7 caenorhabdi
12	163	7.4	4262	2	Q685J2	Q685J2 homo sapien
13	163	7.4	4493	2	Q685J3	Q685J3 homo sapien
14	160.5	7.3	477	2	Q14887	Q14887 homo sapien
15	157.5	7.1	2448	2	Q8WQ05	Q8WQ05 homo sapien
16	156.5	7.1	328	2	Q00446	Q00446 homo sapien
17	155.5	7.0	769	2	Q17921	Q17921 caenorhabdi
18	154.5	7.0	784	2	Q6C185	Q6C185 yarrowia li
19	154	7.0	534	2	Q94317	Q94317 schizosacch
20	151.5	6.9	1240	1	YQ93 CAEEL	Q9X550 caenorhabdi
21	150.5	6.8	382	2	Q9XZ88	Q9XZ88 litomosoid
22	150.5	6.8	797	1	VGLX EHV1B	Q28968 equine herp
23	150.5	6.8	797	2	Q6DL00	Q6DL00 equid herpe
24	150.5	6.8	860	1	CH12 COCTM	P54197 coccidioid
25	149.5	6.8	5179	1	MUC2_HUMAN	Q02817 homo sapien
26	149.5	6.8	5703	1	MUSB_HUMAN	Q9HC84 homo sapien
27	149	6.7	943	1	YL61 SCHPO	Q8TF99 schizosacch
28	148.5	6.7	791	2	Q68VC3	Q68VC3 equid herpe
29	148.5	6.7	1233	1	MUSA_HUMAN	P98088 homo sapien
30	148	6.7	513	2	Q6V4A2	Q6V4A2 drosophila
31	148	6.7	2299	2	Q6A564	Q6A564 bacteroides

32	147.5	6.7	790	2	Q20599	Q20599 caenorhabdi
33	147.5	6.7	842	1	Q95QF5	Q95QF5 caenorhabdi
34	147.5	6.7	1609	2	F1G2 YEAST	P25653 saccharomyc
35	147	6.6	662	1	MUC1_XENLA	Q05049 xenopus lae
36	146	6.6	316	2	Q8VOM4	Q8VOM4 equid herpe
37	146	6.6	457	2	Q86AK1	Q86AK1 dictyosteli
38	146	6.6	472	2	Q6BHG8	Q6BHG8 debaryomyce
39	146	6.6	786	1	STUB_DROME	Q05319 drosophila
40	145.5	6.6	629	2	Q24017	Q24017 drosophila
41	145.5	6.6	716	2	Q9NYE4	Q9NYE4 homo sapien
42	145.5	6.6	901	2	Q6CAJ2	Q6CAJ2 yarrowia li
43	145	6.6	425	2	Q702W3	Q702W3 human herpe
44	145	6.6	1079	2	Q9N4S7	Q9N4S7 caenorhabdi
45	144.5	6.5	377	2	Q8TAX7	Q8TAX7 homo sapien

## ALIGNMENTS

RESULT 1  
MNS1\_HUMAN STANDARD; PRT; 431 AA.  
AC Q9H8J5; ORNECI;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE MNSC domain containing protein 1 precursor (UNQ316/PRO361).  
GN Name=MNSC1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta; DOI=10.1038/ngl285;  
RX PubMed=14702039; DOI=10.1038/ngl285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45 (2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Sehadiri S., Simmons L., Singh J., Smith V., Stinson J., Vagtes A.,  
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.,  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.",  
RL Genome Res. 13:2265-2270(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Contains 1 MANSC domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AK023622; BAB14621.1; -;  
DR EMBL; AY358563; AAQ88926.1; -;  
DR EMBL; BC032998; AAH32998.1; -;  
DR Genbank; HGNC:25505; MANSC1.  
DR InterPro; IPR011106; MANSC\_N.  
DR Pfam; PF07502; MANSC; 1.  
DR PROSITE; PS0986; MANSC; 1.  
KW Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 26 Potential.  
FT CHAIN 27 431 MANSC domain containing protein 1.  
FT DOMAIN 27 385 Extracellular (Potential).  
FT TRANSMEM 386 408 Potential.  
FT DOMAIN 409 431 Cytoplasmic (Potential).  
FT DOMAIN 33 117 MANSC.  
FT DOMAIN 237 332 Thr-rich.  
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 251 251 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 327 327 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 55 55 V -> I (in Ref. 3).  
SQ SEQUENCE 431 AA; 46810 MW; 189136416F0F89AE CRC64;  
Query Match 100.0%; Score 2211; DB 1; Length 431;  
Best Local Similarity 100.0%; Pred. No. 3.3e-136;  
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFFGEGSLTYTLVLCFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIKRGNEPVTSTQ 60

Db 1 MFFGEGSLTYTLVLCFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIKRGNEPVTSTQ 60  
QY 61 EDICNSCCSTKNISGDKACNLMIFDTRKTARQNCVLFPCNEEACPLKPAKGLMSYRII 120  
Db 61 EDICNSCCSTKNISGDKACNLMIFDTRKTARQNCVLFPCNEEACPLKPAKGLMSYRII 120  
QY 121 TDFPSLTRNLPSQELPQEDSLHGHQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
Db 121 TDFPSLTRNLPSQELPQEDSLHGHQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSD 180  
QY 181 HLEKLFKMDSEASQALLAYKEKHSQSFSQSDQEIHLHPENVSALPATVAVASPHHTSA 240  
Db 181 HLEKLFKMDSEASQALLAYKEKHSQSFSQSDQEIHLHPENVSALPATVAVASPHHTSA 240  
QY 241 TPKPATLLPNASVTPSGTSQPOLATAPPTVTTSQPTTLSTVFTRAAATLQAMATT 300  
Db 241 TPKPATLLPNASVTPSGTSQPOLATAPPTVTTSQPTTLSTVFTRAAATLQAMATT 300  
QY 301 AVLTTFQAPTDKSGSLTETIPFTEISNLTNGVYNPTALSMSNVESSTMNKTASWEGR 360  
Db 301 AVLTTFQAPTDKSGSLTETIPFTEISNLTNGVYNPTALSMSNVESSTMNKTASWEGR 360  
QY 361 EASFGSSSQSVPEVGYLPFEKWLIGSLFGVLFVIGLVLLGRILSSSLRKRYSRL 420  
Db 361 EASFGSSSQSVPEVGYLPFEKWLIGSLFGVLFVIGLVLLGRILSSSLRKRYSRL 420  
QY 421 DYLLINGIYVDI 431  
Db 421 DYLLINGIYVDI 431  
RESULT 2  
MSL MACFA STANDARD; PRT; 431 AA.  
ID \_MACFA  
AC Q95KG7;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE MANSC domain containing protein 1 precursor (QtrA-13483).  
GN Name=MANSC1;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.,  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.",  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Contains 1 MANSC domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AB060888; BAB46892.1; -;  
DR InterPro; IPR011106; MANSC\_N.  
DR Pfam; PF07502; MANSC; 1.  
DR PROSITE; PS0986; MANSC; 1.  
KW Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 26 Potential.  
FT CHAIN 27 431 MANSC domain containing protein 1.  
FT DOMAIN 27 385 Extracellular (Potential).  
FT TRANSMEM 386 408 Potential.  
FT DOMAIN 409 431 Cytoplasmic (Potential).  
FT DOMAIN 33 117 MANSC.  
FT DOMAIN 237 332 Thr-rich.  
FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 251 251 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 327 327 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 55 55 V -> I (in Ref. 3).  
SQ SEQUENCE 431 AA; 46810 MW; 189136416F0F89AE CRC64;

Query Match	91.5%;	Score 2022;	DB 2;	Length 397;
Best Local Similarity	92.1%;	Pred. No. 6.4e-124;		
Matches 397; Conservative	0;	Mismatches 0;	Indels 34;	Gaps 1
Qy	1	MFFGEGSLTYLTVLIIICFTLRLSASQCNLKKSLEDVVIDIQSSLSKGRGNEPVYTSQ	60	
Db	1	MFFGEGSLTYTL-----GIRGNEPVYTSQ	26	
Qy	61	ECINSCSTKNI SGD KACNLMI PDTRKTARQPNCYLFFCPENEACPLKPAKGLMSVRII	120	
Db	27	ECINSCSTKNI SGD KACNLMI PDTRKTARQPNCYLFFCPENEACPLKPAKGLMSVRII	86	
Qy	121	TFPSSLTRNLPSQELPQSDLSLLHGQFSQAVTPLAHHTTDYSKPPTDIISWRDTLSQKFGSSD	180	
Db	87	TFPSSLTRNLPSQELPQSDLSLLHGQFSQAVTPLAHHTTDYSKPPTDIISWRDTLSQKFGSSD	146	
Qy	181	HLEKLFKMDASAQLLAYKEKGHSOSSQSFSSDQIAHLHPENVSALPATVAVASPHPTTSA	240	
Db	147	HLEKLFKMDASAQLLAYKEKGHSOSSQSFSSDQIEIAHLHPENVSALPATVAVASPHPTTSA	206	

Db	207	TPKPATLLFTNASVTPSGTSQPQLATTAPPVTTVTSOPPTLLISTVFTRAAATLQAMATT	2666
Qy	301	AVLTFTTFOAPDTSKGSLETIIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR	3600
Db	267	AVLTFTTFOAPDTSKGSLETIIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR	3266
Qy	361	EASPGSSQGSVPENQYGLPFKEKMLLIGSLFGVLFLVIGLVLLGRILSESLLRKKYSRL	4200
Db	327	EASPGSSQGSVPENQYGLPFKEKMLLIGSLFGVLFLVIGLVLLGRILSESLLRKKYSRL	3666
Qy	421	DYLINGIYVDI 431	
Db	387	DYLINGIYVDI 397	

RESULT 4

MNS1_MOUSE			
ID	MNS1_MOUSE	STANDARD;	PRT; 414 AA.
AC	Q9CR33; Q80V71;		
DC	05-JUL-2004 (Rel. 44, Created)		
DT	05-JUL-2004 (Rel. 44, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	MANSC domain containing protein 1 precursor.		
GN	Name=Mansci;		
OS	Mus musculus (Mouse).		

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum, Colon, and Medulla oblongata;  
 RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakado I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gassterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierki R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Simple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,  
 RA Datchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schmech C., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 CC and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- SIMILARITY: Contains 1 MANSO domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AK018660; BAB31329.1; -;  
 DR EMBL; AK018635; BAB31319.1; -;

DR EMBL; AK033526; BAC28341.1; -;  
 DR EMBL; AK033557; BAC28357.1; -;  
 DR EMBL; AK046837; BAC32892.1; -;  
 DR EMBL; BC039930; AH39930.1; -;  
 DR MGD; MGI:1914979; 9130403P13Rik.  
 DR InterPro; IPR011106; MANSO\_N.  
 DR Pfam; PF07502; MANSO; 1.  
 DR PROSITE; PS00986; MANSO; 1.  
 KW Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 24 Potential.  
 FT CHAIN 25 414 MANSO domain containing protein 1.  
 FT DOMAIN 25 369 Extracellular (Potential).  
 FT TRANSMEM 370 392 Potential.  
 FT DOMAIN 393 414 Cytoplasmic (Potential).  
 FT DOMAIN 393 414 MANSO.  
 FT CARBOHYD 128 128 N-linked (GLNAC... ) (Potential).  
 FT CARBOHYD 234 234 N-linked (GLNAC... ) (Potential).  
 FT CARBOHYD 335 335 N-linked (GLNAC... ) (Potential).  
 FT CONFLICT 11 13 SLI -> ALV (in Ref. 2).  
 FT CONFLICT 56 56 L -> V (in Ref. 2).  
 FT CONFLICT 63 63 I -> V (in Ref. 2).  
 FT CONFLICT 139 139 F -> S (in Ref. 2).  
 FT CONFLICT 170 170 R -> G (in Ref. 2).  
 FT CONFLICT 192 192 M -> T (in Ref. 2).  
 FT CONFLICT 242 242 E -> A (in Ref. 2).  
 FT CONFLICT 275 275 G -> A (in Ref. 2).  
 SQ SEQUENCE 414 AA; 44822 MW; 29BB9197C916BA8E CRC64;  
 Query Match 52.7%; Score 1164.5; DB 1; Length 414;  
 Best Local Similarity 59.9%; Pred. No. 6.1e-68;  
 Matches 258; Conservative 37; Mismatches 119; Indels 17; Gaps 6;  
 QY 1 MFRGGSLTYLVITLFLTLRLSASQCNLKSLEDVWIDIQSLSGKRGNEPVYSTQ 60  
 DB 1 MLFRGT-SLAYSIVISFLTPRSAGQCNLTSLSDVWIDIQSLSGKRGNEPIHLATQ 59  
 QY 61 EDCINSCSTKNI-SGDKACNLMIFDTRKTARQPCNLYFFCPNEBACPLKPAKGLMSYRII 120  
 DB 60 EDCIGACCSKDIAGDKACNLMIFDTRKTDRQPCNLYFFCPSEBACPLKPAKGLVTVRLI 119  
 QY 121 TDFPSLTRNPQSELPOEDSLHGGQSQAVTPIAHHTDYSKPTDISWRITLSQKFSDD 180  
 DB 120 RDPFLTSANSSLOOLTQGEFLLDHSPGATPGFRTAGYKPKTGLSWSRSLKSTAPL 179  
 QY 181 HLKELFKMDERASQALLAYKEKHSQSSQFSSDDEIAHLHPENVSALPATVAVASPHSTSA 240  
 DB 180 HLKRLIKADSTMQQL--PEEKSHSQSLQSLSELMKMAHLLEKTVPTPTTVAAPLRNVA 237  
 QY 241 TPKPATLLPTNASVTPSGTSQPLATTAPPVTVTSQPTTLISTVTFRAAATLQAWATT 300  
 DB 238 TLKPELLL-TSISVTAKTAKQE-ATTASPVTVTSKLPVPGVSTSTFT-----PVVTHQ 289  
 QY 301 AVLTTPQATDSKGSLETTPTFEISNLTGNTGVNPTALSMSNVESSTMNKTASWEGR 360  
 DB 290 AALTNTPTAHTDSKGIETMPFQGGSTLT-----SDPRHGKSTSESSITNKTASWEDR 343  
 QY 361 EASPGSSSQSVENQYGLDPKWLIGSLFLGVLFLVIGLVLGRILSLSLRKRYSL 420  
 DB 344 RVSGSASLNKPGSQHGLSFEKWLIGLTLGLVFLVIGLVLGRMLVEALRKRYSRL 403  
 QY 421 DYLINGIYVDI 431  
 DB 404 DYLINGIYVDI 414  
 RESULT 5  
 Q8K010 PRELIMINARY; PRT; 194 AA.  
 ID Q8K010  
 AC Q8K010;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MANSO protein (fragment).

GN Name=Mansci;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC01372; AAH31372.1; -  
 DR MGD; MGI:1914379; Mansci.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 FT NON TER 1  
 SQ SEQUENCE 194 AA; 20701 NW; 11C1F299E1FB3C44 CRC64;

Query Match 22.7%; Score 503; DB 2; Length 194;  
 Best Local Similarity 59.5%; Pred. No. 3.5e-25;  
 Matches 122; Conservative 13; Mismatches 56; Indels 14; Gaps 4;  
 QY 227 PATVAVASHTTSATPKPATLLPTNASVTPGTSOPQATAPPVTTVTSQPTTLSTV 286  
 DB 4 PTTVAVAPLRNVSATLKPALL-TSISVATKTKKE-ATTPASPTVTSKLPVPGSTS 61  
 QY 287 FTAAATLQAMATTAVLTTFQAPTDKSGSLETIPFTISNLTNGVNPATLSMSNV 346  
 DB 62 FT-----PVVTHQAALNTFQHTDSKGLTETPFQGSTLT-----SDPRHCKSSTS 109  
 QY 347 ESSTWNKTASWEGREASPGSSQGVNPNQYGLPPEKMLLIGSLFGLVFLVIGLVLR 406  
 DB 110 ESSITNKTASWEDRRVSGASLNKPKSGHLSPEKMLLIGTLGVLVIGLVLR 169  
 QY 407 ILSESILRRKYSRLDYLINGIYVDI 431  
 DB 170 MLVEALRRKYSRLDYLINGIYVDI 194

RESULT 6  
 Q8VCP2 PRELIMINARY; PRT; 392 AA.  
 AC Q8VCP2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE 1810055G02Rik protein.  
 GN Name=1810055G02Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Liver;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019471; AAH19471.1; -  
 DR MGD; MGI:1919306; 1810055G02Rik.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 SQ SEQUENCE 392 AA; 41081 NW; 1D7996C791211FA CRC64;  
 Query Match 8.9%; Score 197.5; DB 2; Length 392;  
 Best Local Similarity 26.5%; Pred. No. 7.3e-05;  
 Matches 89; Conservative 37; Mismatches 115; Indels 95; Gaps 14;  
 QY 156 HHTDYSKPTDTSWRDTSLSQKFGSSDHLKLFKMDASQALLAYKEKHSQSQF----- 209  
 DB 88 HGTNTSTP-----TREGTDRV-----TSRTLAAPTSSGSSAEQTRPTTIA 130  
 QY 210 ---SSDQIEAHLLENUSALPAT--VAVASPHTT-----SATPKPATLLPTN 251  
 DB 131 GLPSTSTPHAEVPRTNASVSPRTAMAAVAPHTATLAAGTNTSDPHTRTPSPAKSTPTD 190  
 QY 252 -ASVTPSGTSQPLATTAPPVTT-----VTSQPTTLISTVFTRAAAT 293  
 DB 191 TSSKNPIPTSGAQIGTQVLTQDPVHSTAGRSALSPSNATLEPTTQVQTK-EPSAST 249  
 QY 294 LQAMATTAVLTTFQAPTDKSGSLETIPFTISNLTNGVNPATLSMSNVESSTWNK 353  
 DB 250 VPARATSLSPDWDVTSPTTQPS--PTLP-----TQGTGG--PGTLTTEQVGKTTSG 298  
 QY 354 TASWEGREASPGSSQGSV-----PENQYGLPFE-----KWLIGSLLPV 394  
 DB 299 TAS-----AGPTSRSSGDIKVPTTDSQPSQGYLVITDALTPSLVNKMLLVLLGV 353  
 QY 395 LFLVIGLVLLGRILSLSLRKYSRLDYLINGIYVD 430  
 DB 354 TLFTAVLVMPALQAYESYKKDYTQVDYLINGYAD 389  
 RESULT 7  
 Q9H2K4  
 ID Q9H2K4 PRELIMINARY; PRT; 449 AA.  
 AC Q9H2K4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)





Query Match 8.9%; Score 196.5; DB 2; Length 392;  
 Best Local Similarity 26.1%; Pred. No. 8.4e-05;  
 Matches 88; Conservative 42; Mismatches 110; Indels 97; Gaps 15;

QY 156 HHTDYSKPTDISWRDLSOKFGSLHLEKFLKMDASACALLAYKEKGHSQSQFSSDQRI 215  
 DB 88 HGTNTSTPT-----TREGTTRV-----TSKTLAVTSSGSSAEQTRPTTI 129

QY 216 AHL-----LPE-NVSALPAT--VAVASPHTT-----SATPKPATLLPT 250  
 DB 130 AGLPSLSTPHAEPRTNASVSRTAMATVAHTATLAAGTVNTSDPHRTTSPAKSIPT 189

QY 251 N-ASVTPSGTSPQLATAPPVTT-----VTSOPPTLLISTVTRAAA 292  
 DB 190 DTSSKNPIPTSGAQIGTIVQLTTPQVHSTAGRSALSPSNATLEPTTTQVQTK-EPAS 248

QY 293 TLQAMATTAVLTTFQAPTDKSGSLETIPFTEISNLTNTGNVNPATLSMNSVSSTMN 352  
 DB 249 TVPARATLSPPVDVISPITQPS--PTLP-----TQGTGG--PGTLLTTTQVGTKITS 297

QY 353 KTASMEGRASPGSSQSGSV-----PENQVGLPFE-----KWLIGSLIFG 393  
 DB 298 GTAS-----AGTSRSSGDIKVTPTDSCQPSQGQVLTIDALTSLVNMKLLVLLVVG 352

QY 394 VLFLVIGLVLLGRILSESRLRKRYRLDYLINGIYVD 430  
 DB 353 VTLFIAVLVWFALQAYESYKKDYQTDVYDLINGMYAD 389

RESULT 9  
 Q96F05 PRELIMINARY; PRT; 449 AA.

AC Q96F05; TISSUE=Skin;  
 DT 01-DEC-2001 (TreeBLrel. 19, Created)  
 DT 01-DEC-2001 (TreeBLrel. 19, Last sequence update)  
 DT 25-OCT-2004 (TreeBLrel. 28, Last annotation update)  
 DE Chromosome 11 open reading frame 24 (FP2568) (C11orf24).  
 GN Name=C11orf24; ORFNames=UNQ1872;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,  
 RA Wan D.F., Gu J.R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270 (2003).  
 DR EMBL; BC011765; AAH11765.1; -  
 DR EMBL; AF370372; AAQ15208.1; -  
 DR EMBL; AY358754; AAO89114.1; -  
 DR Genew; HGNC:1174; C11orf24.  
 DR InterPro; IPR001395; Aldoc/ket\_red.  
 DR PROSITE; PS00063; ALDOXETO\_REDUCTASE\_3; UNKNOWN 1.  
 SQ SEQUENCE 449 AA; 46142 MW; BF984AA360FC415 CRC64;

Query Match 8.5%; Score 188; DB 2; Length 449;  
 Best Local Similarity 22.0%; Pred. No. 0.00036;  
 Matches 116; Conservative 49; Mismatches 167; Indels 196; Gaps 18;

QY 13 LVIIICFLRLSASQCLKSLIEDVVIDIQSLSKIRGNEPVYTSIOEDCINSCSTKN 72  
 DB 5 LVLIWIFSLSESSEHAASNDPRNFVPMKMKLVKRNASVEIVDNKTSIEDVTMAAS --- 61

QY 73 ISGDKACNLMIFDRKTKARQPCNYLFFCPNBEACPLKPAKGLMSYRIITDPFSLRNPLS 132  
 DB 62 -----PVLTKG-----TSAHLNS 76

QY 133 QELPQEDSLHGHQSQAVTPLAHHHTDYSKPTDISWRDLSQKFGSSDHLKFLKMDAS 192  
 DB 77 MEVTTEDT-----SRTDVSEP-----ATSGVAADGVTSIAPTAVAS 112

QY 193 AQLLAYKEKHSQSQSQFSSDOEIAHLHPENVSALPATVAVASPHT-----TSATPKPATL 247  
 DB 113 STTAA-----SITTAASMTVASSAP-TTAASSTTVASIAPTTAASMTAASSTPMTL 164

QY 248 ---LPTNASV--TPS--GTSQFQLATAPPVTTVTTSQPTLLISTVFTTAAATLQAMAT 300  
 DB 165 ALPAPTSTGTGTSTTATGHPSLSTALAQVPKSSALPRATLATLATRA-----QTVAAT 220

QY 301 A-----VLTTFQAPTDKSG 315

DB 251 ANTSPMSTRSPSKHMPSDTAASVPVPMRPOAQGPISQVSDQPVVNTNKSTPMPSNT 280

QY 316 SLEITPFTFTEISNLTNTGNVNPATL-----SMS-NVESSTNMKTASWEG- 359  
 DB 281 TPEAPPTTV--VTTTKAQAREPTASVPVPHSTPIPEMEAMSPPTQSPMPYTORAAGP 338

QY 360 -----REASPGSSQSQSVPENQYG--LP-----FE 382  
 DB 339 GTSQAPEQVETEATPGTDSTGTPTSSSGTKMPATDSQCPSTQGGYVWVVTTEPLTQAVVD 398

QY 393 KWLIGSLIFGLVIGLVLLGRILSESRLRKRYRLDYLINGIYVD 430  
 DB 399 KTLALLVLLGLVTLFIVLVLFALQAYESYKKDYQTDVYDLINGMYAD 446

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 ID Q8WWQ4  
 AC Q8WWQ4;  
 PRELIMINARY; PRT; 1349 AA.







QY 341 LSMSNVESSTWNTKASWEGREASPGSSSGS 371  
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RESULT 15

Q8MWQ5  
ID Q8MWQ5 PRELIMINARY; PRT; 2448 AA.  
AC Q8MWQ5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mucin 5 (Fragment).  
GN Name=MUC5AC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Trachea;  
RX MEDLINE=21428417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;  
RA Escande F., Aubert J.P., Porchet N., Buisine M.P.;  
RT "Human mucin gene MUC5AC: organization of its 5'-region and central  
repetitive region.";  
RL Biochem. J. 358:763-772(2001).  
DR EMBL; AJ298317; CAC83674.1; -.  
DR HSPF; P56682; ICCV.  
DR Genew; HGNC:7515; MUC5AC.  
DR Pfam; PF01826; TIL; 2.  
DR Pfam; PF00094; VWD; 3.  
DR SMART; SM00214; VWC; 3.  
DR SMART; SM00216; VWD; 3.  
DR PROSITE; PS00527; RIBOSOMAL\_S14; UNKNOWN\_2.  
FT NON TER 2448 2448  
SQ SEQUENCE 2448 AA; 260968 MW; ASC1BD62784D952 CRC64;

Query Match 7.1%; Score 157.5; DB 2; Length 2448;

Best Local Similarity 23.1%; Pred. No. 0.29; Gaps 16;  
Matches 87; Conservative 38; Mismatches 142; Indels 109; Gaps 16;

QY 63 CIN-----SCSTKNISGDKACNLMI FDRKTARQPNLCYLFCCPNEACPLKPAKGLMSY 117  
DB 2034 CYNVEIRIQCCETVNV-----CRDITRPKTVATTRTPH-----PTGAQTQT 2076  
QY 118 RIITDFSLRNLP---SOELPQEDSLLHGQFSQAVTFLAHHTDYSKPTDISW----- 168  
DB 2077 TFTTHMPSASTEQTATSRGGTATSVTQGTHTTPVTRNCHPRCTWTWTFDVPDPSPGPH 2136  
QY 169 ---RDTLSQKFGSDHLEKLFKMDASAQMIAYKEGHSOSS-----QFSSDQ----- 213  
DB 2137 GGDKEYNNIRSG---EKICRRPEEITRLQC-RAKSHPEVSIHGLGVQVQCSREGLVC 2192  
QY 214 -----ETIAHLLPENVSALPATVAVASPHHTSATPKPATLIPNTAS----- 253  
DB 2193 RNQDQGFPMCLNIEVRVLCCEPKGCPVT---STPVTAPSPSGRAISPTQSTSSWQK 2249  
QY 254 -----VTPGTSQPOLATT-----AP-----PVTTVTSQPTTLISVFTFAA 291  
DB 2250 SRTTLVTSTSTPQSTVAHTTSTTSAPTARTSAPTSTTSVPTTSTISGPKTTPS 2309  
QY 292 ATLQAMATVLTTFQATDTSKGSLETIPFTEISNLTNGVNYNPNTALSMNSVESSTM 351  
DB 2310 PVPTTSTTSATTTISAPTSTTS---VPCTTSPV-LITSTTSAPT-----TR 2355  
QY 352 NKTASWEGREASPGSS 367  
DB 2356 TTSASPAGTSGPGNT 2371

Search completed: April 26, 2005, 21:51:30  
Job time : 128 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 26, 2005, 21:59:56 ; Search time 4716 Seconds  
(without alignments)  
4428.371 Million cell updates/sec

Title: US-10-735-014-83

Perfect score: 2211

Sequence: 1 MFPGEGSLTYLTVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sv.\*
- 13: gb.un.\*
- 14: gb.vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2211	100.0	2284	6	BD140585
2	2211	100.0	2284	6	AR252736
3	2211	100.0	2284	6	AR429104
4	2211	100.0	2284	6	AR534995

5	2211	100.0	2284	6	AX403627	Sequence
6	2211	100.0	2284	9	AY358563	BD160088 Homo sapi
7	2211	100.0	2297	6	BD160088	Primer fo
8	2211	100.0	2297	6	AX883044	Sequence
9	2211	100.0	2297	9	AK023622	Homo sapi
10	2210	100.0	2333	9	BC032998	Homo sapi
11	2062	93.3	2015	6	BD227259	Secreted
12	2039	92.2	2345	9	AB060888	Macaca fa
13	2022	91.5	2221	6	CQ776818	Primer fo
14	2022	91.5	2221	6	CQ776818	Sequence
15	2022	91.5	2221	9	AX876122	Sequence
16	2022	91.5	2221	9	AK001160	Homo sapi
17	1573.5	71.2	14000	9	AC007621	Homo sapi
18	1573.5	71.2	18834	2	AC131617	Homo sapi
19	1216	55.0	735	6	CQ735543	Sequence
20	1179.5	53.3	2286	10	BC039930	Mus muscu
21	1164.5	52.7	2286	6	CQ777667	Sequence
22	835	37.8	548	6	BD059530	Secreted
23	780.5	35.3	805	6	BD149896	Primer fo
24	780.5	35.3	805	6	AX869834	Sequence
25	764.5	34.6	855	6	BD147198	Primer fo
26	764.5	34.6	855	6	AX867136	Sequence
27	709.5	32.1	110134	2	AC149660	Bos tauru
28	683.5	30.9	224870	2	AC129657	Rattus no
29	683.5	30.9	250782	2	AC128093	Rattus no
30	678	30.7	195959	2	AC126692	Mus muscu
31	678	30.7	236589	2	AC118035	Mus muscu
32	633	28.6	422	6	BD071236	Secreted
33	522	23.6	1627	5	AJ719946	Gallus ga
34	503	22.7	1326	10	BC031372	Mus muscu
35	386	17.5	188344	2	AC131617	Homo sapi
36	338.5	15.3	242590	2	AC133722	Rattus no
37	271.5	12.3	236589	2	AC118035	Mus muscu
38	242	10.9	295	6	AX894034	Sequence
39	242	10.9	295	6	BD029567	Sequence
40	228	10.3	110134	2	AC149660	Bos tauru
41	221	10.0	2165	5	BX929877	Gallus ga
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43	201	9.1	2058	9	AF264781	Homo sapi
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45	197	8.9	112864	2	AC024127	Homo sapi

ALIGNMENTS

RESULT 1	BD140585	BD140585	2284 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	Polypeptides and nucleic acids encoding the same.					
DEFINITION	Polypeptides and nucleic acids encoding the same.					
ACCESSION	BD140585					
VERSION	BD140585.1 GI:23235530					
KEYWORDS	JP 2002505850-A/68.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
TITLE	1 (bases 1 to 2284)					
JOURNAL	Wood, W.I., Goddard, A., Gurney, A.L., Yuan, J., Baker, K.P. and Zheng, J.					
COMMENT	Polypeptides and nucleic acids encoding the same					
	Patent: JP 2002505850-A 68 26-FEB-2002;					
	GENENTECH INC					
	OS Homo sapiens (human)					
	PN JP 2002505850-A/68					
	PF 01-DEC-1998 JP 2000523338					
	PR 03-DEC-1997 US 60/067411, 11-DEC-1997 US 60/069334 PR					
	11-DEC-1997 US 60/069335 11-DEC-1997 US 60/069278 PR					
	12-DEC-1997 US 60/069425, 16-DEC-1997 US 60/069696 PR					
	16-DEC-1997 US 60/069694, 16-DEC-1997 US 60/069702 PR					
	17-DEC-1997 US 60/069870, 17-DEC-1997 US 60/069870 PR					
	18-DEC-1997 US 60/068017, 05-JAN-1998 US 60/070440 PR					
	09-FEB-1998 US 60/074086, 09-FEB-1998 US 60/074092 PR					

25-FEB-1998 US 60/075945  
PI WILLIAM I WOOD, AUDREY GODDARD, AUSTIN L GURNEY, JEAN YUAN, KEVIN  
P BAKER  
PI JIAN ZHENG  
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC  
C12P21/02,  
PC C12P21/08, C12Q1/68, C12N15/00, C12N5/00  
CC Polypeptides and nucleic acids encoding the same PH Key  
Location/Qualifiers  
FT source 1..2284  
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Alignment Scores:  
Pred. No.: 5,79e-112 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-735-014-83 (1-431) x BD140585 (1-2284)

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Db 226 ATGTTCTCGGGGAGAGGAGCTTACCTTTGGTAATAATTTGCTTCTCGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuIleValSerLeuGluAspValIleLeu 40  
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Qy 41 IleGlnSerLeuSerLeuGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
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Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
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LOCUS AR252736 Sequence 514 from patent US 6478825.  
DEFINITION AR252736  
ACCESSION AR252736  
VERSION AR252736.1 GI:27300644  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2284)  
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 514 12-NOV-2002;  
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Alignment Scores:  
Pred. No.: 5,79e-112 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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US-10-735-014-83 (1-431) x AR252736 (1-2284)

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 DEFINITION Sequence 82 from patent US 6642360.  
 ACCESSION AR429104  
 VERSION AR429104.1 GI:40189199  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM  
 Unclassified.  
 REFERENCE 1 (bases 1 to 2284)  
 AUTHORS Filvaroff, E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L.  
 and Wood, W.I.  
 TITLE Secreted polypeptides that stimulate release of proteoglycans from cartilage  
 JOURNAL Patent: US 6642360-A 82 04-NOV-2003;  
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 Pred. No.: 5,79e-112 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 DB 226 ATGTTCTTCGGGGAGAGAGCTTGAACCTTACCTTTGGTATAATTTGCTTCTGACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLeuLysSerLeuGluAspValIleAsp 40  
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DEFINITION Sequence 82 from patent US 6734288.
ACCESSION AR534995
VERSION AR534995.1 GI:53925785
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
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REFERENCE 1 (bases 1 to 2284)
AUTHORS Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.I.
and Wood,W.I.
TITLE Antibodies against a secreted polypeptide that stimulates release
of proteoglycans from cartilage
JOURNAL Patent: US 6734288-A 82 11-MAY-2004;
FEATURES Location/Qualifiers
source 1. 2284
/organism="unknown"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 5,79e-112 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-735-014-83 (1-431) x AR534995 (1-2284)
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Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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AX403627 2284 bp DNA linear PAT 14-JUN-2002  
 LOCUS Sequence 514 from Patent WO0073454.  
 DEFINITION AX403627  
 ACCESSION AX403627  
 VERSION AX403627.1 GI:21437090

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,  
 Ferrara, N., Gerber, H., Gertitsen, M., Goddard, A., Godowski, P.,  
 Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
 Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
 Williams, P., Wood, W.I. and Zhang, Z.  
 Secreted and transmembrane polypeptides and nucleic acids encoding  
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## JOURNAL

Patent: WO 0073454-A 514 07-DEC-2000;  
 Genentech Inc. (US)

## FEATURES

source

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## ORIGIN

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Pred. No.: 5.79e-112 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
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US-10-735-014-83 (1-431) x AX403627 (1-2284)

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 VERSION AY358563.1 GI:37182247  
 KEYWORDS FLI CDNA.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (Bases 1 to 2284)  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)

## TITLE

12975309  
 2 (Bases 1 to 2284)  
 Clark,H.F.

## JOURNAL

PUBMED  
 12975309

## AUTHORS

Clark,H.F.

## TITLE

Direct Submission

## JOURNAL

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

## FEATURES

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## gene

## CDS

## Alignment Scores:

Pred. No.: 5.79e-112 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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US-10-735-014-83 (1-431) x AY358563 (1-2284)

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## RESULT 7

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 DEFINITION  
 ACCESSION BD160088  
 VERSION 1 GI:27865846  
 KEYWORDS JP 2002191363-A/14931.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2297)  
 Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto.J.,  
 Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K. and Otsuki.T.  
 TITLE Primer for synthesizing full-length cDNA and use thereof  
 JOURNAL Patent: JP 2002191363-A 14931 09-JUL-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002191363-A/14931  
 PD 09-JUL-2002  
 PF 28-JUL-2000 JP 2000280990  
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU  
 SAITO,  
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
 PI KEIICHI NAGAI, TETSUJI OTSUKI  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
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## FEATURES

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 DEFINITION Sequence 17949 from Patent EP1074617.  
 ACCESSION AX883044  
 VERSION AX883044.1 GI:40037945  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,  
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.  
 TITL Primers for synthesising full-length cDNA and their use  
 JOURNAL Patent: EP 1074617-A 17949 07-FEB-2001;  
 Research Association for Biotechnology (JP)  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 5,82e-112 Length: 2297  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-735-014-83 (1-431) x AX883044 (1-2297)

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DEFINITION	Homo sapiens cDNA FLJ13560 fis, clone PLACE1007877.			
ACCESSION	AK023622			
VERSION	AK023622.1	GI:10435603		
KEYWORDS	oligo capping; fis (full insert sequence).			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Eukaryotica; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hottuta, T., Kusanagi, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aocuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujihara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiroo, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.			
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs			
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)			
PUBMED	14702039			
REFERENCE				
AUTHORS	Isogai, T., Ota, T., Hayaashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakanatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.			
TITLE	NEDO human cDNA sequencing project			
JOURNAL	Unpublished			
REFERENCE	3 (bases 1 to 2297)			
AUTHORS	Isogai, T. and Otsuki, T.			
TITLE	Direct Submission			
JOURNAL	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@nri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)			
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.			
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Score:	2211.00	Matches:	431	
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 1 (bases 1 to 2333)  
 Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshnyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 REFERENCE 2 (bases 1 to 2333)  
 Strausberg,R.  
 Direct Submission  
 Submitted (21-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
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 COMMENT NTH-MGC Project URL: http://mgc.nci.nih.gov  
 On Aug 25, 2003 this sequence version replaced gi:21542502.  
 Contact: MGC help desk  
 Email: gcgaps-x@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshitaki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
 http://www.systemsbio.org  
 contact: amadan@systemsbiology.org  
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 33 Row: h Column: 14  
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KEYWORDS JP 2002522062-A/20.			
SOURCE Homo sapiens (human)			
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
JACOBS, K., MCCOY, J. M., LAVALLIE, E. R., RACIE, L. A. C., EVANS, C.,			
MERBERG, D., TREACY, M., AGOSTINO, M. J., II, R. J. S., SPAULDING, V.,			
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Patent: JP 2002522062-A 20 23-JUL-2002;			
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OS Homo sapiens (human)			
PN JP 2002522062-A/20			
PD 23-JUL-2002			
PF 13-AUG-1999 JP 2000565001			
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04-SEP-1999 US 60/099229,23-OCT-1998 US 60/105368 PR			
08-JAN-1999 US 60/115234,12-FEB-1999 US 60/119931 PR			
18-FEB-1999 US 60/120575,30-APR-1999 US 60/132020 PR			
11-AUG-1999 US 60/148424			
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A COLLINS			
PI RACIE,			
PI CHERYL EVANS,DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,			
PI ROBERT J STEININGER II,VIKKI SPAULDING,GORDON G WONG,HILARY F			
PI CLARK,			
PI KIM RECHTEL			
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AUTHORS		Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.	
TITLE		Isolation of full-length cDNA clones from macaque brain CDNA libraries	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 2345)	
AUTHORS		Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.	
TITLE		Direct Submission	
JOURNAL		Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	
COMMENT		(E-mail:khashienih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)	
		Lab host: TOP10	
		Vector: pME18S-FL3 (Acc.No. AB009864)	
		R. Site1: DraIII (CACTGTGTG)	
		R. Site2: DraIII (CAACATGTG)	
		Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGAGGCTCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method	
		(Sugano et al., , Institute of Medical Science, University of Tokyo).	
FEATURES		Custom primer used for sequencing	
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ORIGIN
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US-10-735-014-83 (1-431) x AB060888 (1-2345)

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DB      615 AGAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCAAGAGTTACCCAGGAGGACTCT 674

QY      141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspThr 160
DB      675 CTCCTACCTGGCCAGTTTTCACAGCAGCTCACTCTCTAGCCCGTCATCACATAGTTTAT 734

QY      161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB      735 TCAAAGCCCAACCGATATCTCATGGAGAGAGACACTTCTCAGAAGTTTGGATCTCCAGAT 794

QY      181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaThrLysGlu 200
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QY      201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluLleAlaHisLeuLeuPro 220
DB      855 AAAAGCCCATCTTCAGAGTTTCAGAGTTTCTCTGTATCAAGAAATAGCTCATCTGCTGCT 914

QY      221 GluAsnValSerAlaLeuProAlaThrValAlaAlaSerProHisThrThrSerAla 240
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QY      261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280
DB      1035 CAGCCACAGCTGGCCACCATCTCCGCTGTAAACACACTGTCACTTCTCAGCCTCCACG 1094

QY      281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThr 300
DB      1095 ACCCTCATTTCTACAGTTTACACGGGCTGTGGCTACTCCACAGCAATGGCTACACA 1154

QY      301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB      1155 GCAGTTCTGACTTACCACCTTTTCAGGCACCTTACGGACTTGAAGGCGACCTAGAAACGATA 1214

QY      321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340
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QY      341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
DB      1275 CTTTCTATGTCAATGTGAAGTCTTCGCTACGATATAAACTGCTTCTTGGGAGGTAGG 1334

QY      361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnThrGlyLeuPro 380
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QY      381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
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QY      401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
DB      1455 CTCGTCCTCTCGGGGAGATCTCTCGGAATCACTCCGACGAAACACTTACTCAAGACTG 1514

QY      421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 13
BD155963      2221 bp      DNA      linear      PAT 17-JAN-2003
LOCUS      Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION      BD155963
VERSION      BD155963.1 GI:27861721
KEYWORDS      JP 2002191363-A/10806.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2221)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 10806 09-JUL-2002;
HELIX RESEARCH INSTITUTE
QS Homo sapiens (human)
PN JP 2002191363-A/10806
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC
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Primer for synthesizing full-length cDNA and use thereof FH Key
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FT CDS
Location/Qualifiers

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US-10-735-014-83 (1-431) x BD155963 (1-2221)

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Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
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Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
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Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 704 CACTTGGAGAAACTATTATTAAGATGGATGAAGCAGTGCACAGCTCCTTGCTTATAAGGAA 763

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Db 1364 CTCGTCCTCTGGGTAGATCCTCTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1423
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LOCUS COQ776818 2221 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 504 from Patent EP1394274.
ACCESSION COQ776818
VERSION COQ776818.1 GI:45380208
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuwara, K.
TITLE Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL Patent: EP 1394274-A 504 03-MAR-2004;
Genex Research, Inc. (JP)
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  Score:        92.11%      Conservative: 0
  Percent Similarity: 92.11% Mismatches: 0
  Best Local Similarity: 92.11% Indels: 34
  Query Match: 91.45%      Gaps: 1
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US-10-735-014-83 (1-431) x COQ776818 (1-2221)

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Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
Db 304 ----- 304

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DEFINITION AX876122
ACCESSION AX876122
VERSION AX876122.1 GI:40030858
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 11027 07-FEB-2001;
Research Association for Biotechnology (JRP)
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ORIGIN
Alignment Scores:
Pred. No.: 1,19e-101 Length: 2221
Score: 2022.00 Matches: 397
Percent Similarity: 92.11% Conservatives: 0
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GenCore version 5.1.6  
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Run on: April 26, 2005, 21:54:06 ; Search time 604 Seconds  
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Title: US-10-735-014-83

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Delop 6.0 , Delext 7.0

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Listing first 45 summaries

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- 7: Geneseq\_2002bs:\*
- 8: Geneseq\_2003as:\*
- 9: Geneseq\_2003bs:\*
- 10: Geneseq\_2003cs:\*
- 11: Geneseq\_2003ds:\*
- 12: Geneseq\_2004as:\*
- 13: Geneseq\_2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2211	100.0	2284	2 AAX80059	Aax80059 Human PRO
2	2211	100.0	2284	3 AAX49567	Aax49567 Human PRO
3	2211	100.0	2284	5 AAF44268	Aaf44268 Human PRO
4	2211	100.0	2284	8 ACA64519	ACA64519 Novel hum
5	2211	100.0	2284	8 ABX96832	Abx96832 Human cDN

6	2211	100.0	2284	8 ABX78486	Abx78486 DNA encod
7	2211	100.0	2284	8 ABX77120	Abx77120 cDNA enco
8	2211	100.0	2284	8 ABX80978	Abx80978 Human sec
9	2211	100.0	2284	8 ACD44487	ACd44487 cDNA enco
10	2211	100.0	2284	8 ABX75951	Abx75951 Human cDN
11	2211	100.0	2284	8 ABX89662	Abx89662 cDNA enco
12	2211	100.0	2284	8 ABX79658	Abx79658 Human sec
13	2211	100.0	2284	8 ACA93679	ACA93679 Novel hum
14	2211	100.0	2284	8 ABX81361	Abx81361 Novel hum
15	2211	100.0	2284	8 ACA93177	ACA93177 Novel hum
16	2211	100.0	2284	8 ABX17261	Abx17261 Human PRO
17	2211	100.0	2284	8 ABX34148	Abx34148 cDNA enco
18	2211	100.0	2284	9 ACA04368	ACA04368 Human PRO
19	2211	100.0	2284	9 ACA68116	ACA68116 Novel hum
20	2211	100.0	2284	9 ACA88565	ACA88565 Human sec
21	2211	100.0	2284	9 ACD82072	ACd82072 cDNA enco
22	2211	100.0	2284	9 ADA38025	Ada38025 Human cDN
23	2211	100.0	2284	9 ADA21711	Ada21711 Human cDN
24	2211	100.0	2284	9 ADA10498	Ada10498 Human cDN
25	2211	100.0	2284	9 ADA18042	Ada18042 cDNA enco
26	2211	100.0	2284	9 ADA28150	Ada28150 Human cDN
27	2211	100.0	2284	9 ADA94730	Ada94730 Human cDN
28	2211	100.0	2284	9 ADA38955	Ada38955 Human cDN
29	2211	100.0	2284	9 ADA93076	Ada93076 Human cDN
30	2211	100.0	2284	9 ACH65633	ACH65633 Human cDN
31	2211	100.0	2284	9 ADA22637	Ada22637 Human cDN
32	2211	100.0	2284	9 ACD39623	ACd39623 Human cDN
33	2211	100.0	2284	9 ADA06803	Ada06803 Human sec
34	2211	100.0	2284	9 ADA39496	Ada39496 Human cDN
35	2211	100.0	2284	9 ADB96522	ADB96522 Human PRO
36	2211	100.0	2284	10 ADC57994	Adc57994 Human PRO
37	2211	100.0	2284	10 ADC25838	Adc25838 Human cDN
38	2211	100.0	2284	10 ADC25596	Adc25596 Human PRO
39	2211	100.0	2284	10 ADC55358	Adc55358 Human cDN
40	2211	100.0	2284	10 ADC12225	Adc12225 Human cDN
41	2211	100.0	2284	10 ADC56647	Adc56647 Human PRO
42	2211	100.0	2284	10 ADC11692	Adc11692 Human cDN
43	2211	100.0	2284	10 ADC25717	Adc25717 Human cDN
44	2211	100.0	2284	10 ADC14814	Adc14814 Novel hum
45	2211	100.0	2284	10 ADD08346	Add08346 Novel hum

ALIGNMENTS

RESULT 1  
AAX80059  
ID AAX80059 standard; cDNA; 2284 BP.  
XX AC AAX80059;  
XX DT 12-AUG-1999 (first entry)  
XX DE Human PRO361 nucleotide sequence.  
XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;  
XX KW secreted protein; transmembrane protein; inflammation disorder; ss.  
XX OS Homo sapiens.  
XX PN WO9928462-A2.  
XX PD 10-JUN-1999.  
XX PF 01-DEC-1998; 98WO-US025108.  
XX PR 03-DEC-1997; 97US-0067411P.  
XX PR 11-DEC-1997; 97US-0069278P.  
XX PR 11-DEC-1997; 97US-0069334P.  
XX PR 11-DEC-1997; 97US-0069335P.  
XX PR 12-DEC-1997; 97US-0069435P.  
XX PR 16-DEC-1997; 97US-0069694P.  
XX PR 16-DEC-1997; 97US-0069696P.  
XX PR 16-DEC-1997; 97US-0069702P.

PR 17-DEC-1997; 97US-0069870P.  
 PR 17-DEC-1997; 97US-0069873P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 05-JAN-1998; 98US-0070440P.  
 PR 09-FEB-1998; 98US-0074086P.  
 PR 09-FEB-1998; 98US-0074092P.  
 PR 25-FEB-1998; 98US-0075945P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;  
 XX  
 DR WPI; 1999-371118/31.  
 DR P-PSDB; AAY17834.  
 XX  
 PT Nucleic acids encoding PRO secreted and transmembrane proteins.  
 XX  
 PS Claim 2; Fig 36; 123pp; English.  
 CC  
 CC The present invention describes nucleic acids encoding PRO secreted and  
 CC transmembrane proteins used therapeutically. The PRO proteins have  
 CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive  
 CC activity. The proteins and polynucleotides can be used in therapy,  
 CC identification of homologues, raising antibodies and design of probes and  
 CC primers. They can be used in a range of diseases related to proteins that  
 CC they have homology with, e.g. a PRO protein having homology to complement  
 CC proteins may be used in inflammatory responses  
 XX  
 SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservations: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-735-014-83 (1-431) x AAX80059 (1-2284)  
 QY 1 MetPheGlyGlyGluGlySerLeuThrThrLeuValIleCysPheLeuThr 20  
 DB 226 ATGTTCTTCGGGGGAGAGGAGCTGACTTACACTTTGGTAAATTTGCTTCTCCGACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuIleCysLeuGluAspValIleAsp 40  
 DB 286 CTAAGGCTGTCTGCTAGTCAGAAATGGCTCAAAAAGAGCTAGAGAGATGTTGTCATTGAC 345  
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
 DB 346 ATCCAGTCACTCTTTCTAGGGGATCAGAGGCATGAGCCCGTATATATCTCAACTCAA 405  
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 DB 406 GAGACTGCATTAATTTCTGCTGTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 DB 466 TTGATGATCTTCGACACTCGAAAAACAGTAGACACCCCAACTGCTACTTATTTCTGT 525  
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 DB 526 CCCAACGAGGAGGCTGTCCATTGAAACCAACCAAGAGACTTATGAGTTACAGATTAATT 585  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 DB 586 ACAGATTTCCATCTTTGACCAAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCT 645  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160  
 DB 646 CTCTTACATGGCCCAATTTTCAAGACGATCTCTCCCTAGCCCATCATCATCAGATATTAT 705  
 QY 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180

DB 706 TCAAAGCCCAACCATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765  
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
 DB 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCTTGTGTTAAGGAA 825  
 QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGlnIleAlaHisLeuLeuPro 220  
 DB 826 AAAGGCCATTTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTATCTGTGCTCT 885  
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 DB 886 GAAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGCT 945  
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 DB 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCACTGACACCTTCTGGGACTTCC 1005  
 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
 DB 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCTTCCACG 1065  
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 DB 1066 ACCTCATTTCTACAGTTTTCACCGGCTGCGGCTACACTCCCAAGCAATGGCTACAACA 1125  
 QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 DB 1126 GCAGTTCTGACTACCACTTTTACGGCACCTTACGGACTTCGAAAGGCAGCTTAGAAACCAT 1185  
 QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 DB 1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGGAAATGTATATAACCTTACTGCA 1245  
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360  
 DB 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATCAATAAAACTGCTTCTCTGGAGGTAGG 1305  
 QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 DB 1306 GAGGCCAGTCCAGGCGAGTCTCTCCAGGCGAGTGTTCAGAAAATCAGTAGCGGCTTCCA 1365  
 QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 DB 1366 TTTGAAAAATAGGCTTCTATTCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGGTATAGGC 1425  
 QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgLysArgTyrSerArgLeu 420  
 DB 1426 CTCGTCTCTCTGGTGAATCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485  
 QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 DB 1486 GATTATTGATCAATGGATCTATGTGGACATC 1518  
 RESULT 2  
 AAA49567  
 ID AAA49567 standard; cDNA; 2284 BP.  
 XX  
 AC AAA49567;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Human PRO361 cDNA.  
 XX  
 KW PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;  
 KW PRO715; PRO241; PRO323; PRO299; PRO344; PRO347; PRO355; PRO353;  
 KW PRO361; PRO365; transmembrane polypeptide; antibody; screening;  
 KW detection; inhibition; probe; primer; human; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers

```

FT CDS      226..1521
FT          /*tag= a
FT          /product= "PRO361 polypeptide"
XX PN      WO200032776-A2.
XX PD      08-JUN-2000.
XX PF      01-DEC-1999; 99WO-US028301.
XX PR      01-DEC-1998; 98WO-US025108.
XX PR      16-DEC-1998; 98US-0112850P.
XX PR      22-DEC-1998; 98US-0113296P.
XX PA      (GETH ) GENENTECH INC.
XX PI      Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
XX PI      Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
XX PI      Hillan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX DR      WPI; 2000-412324/35.
XX DR      P-PSDB; AAB01325.
XX PT      New human nucleic acids encoding secreted and transmembrane polypeptides,
XX PT      designated as PRO polypeptides, useful as pharmaceutical and diagnostic
XX PS      agents.
XX PS      Claim 2; Fig 31; 187pp; English.
XX CC      New human nucleic acids encoding secreted and transmembrane polypeptides
XX CC      which are designated as PRO polypeptides are described The membrane-bound
XX CC      proteins have various industrial applications, including as
XX CC      pharmaceutical and diagnostic agents. The membrane-bound proteins can
XX CC      also be employed for screening of potential peptide or small molecule
XX CC      inhibitors of the relevant receptor/ligand interaction. Anti-PRO
XX CC      antibodies are useful for the affinity purification of PRO from
XX CC      recombinant cell culture or natural sources
XX SQ      Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,02e-141      Length:      2284
Score:          2211.00      Matches:      431
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              3              Gaps:      0

US-10-735-014-83 (1-431) x AAA49567 (1-2284)

QY      1 MetPhePheGlyGlyGlySerLeuThrThrLeuValleilleCysPheLeuThr 20
DB      226 ATGTTCTTCGGGGAGAGAGGAGCTTACCTTGGTAAATTTGCTTCTGACA 285

QY      21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValleilleAep 40
DB      286 CTAAGGCTCTGCTAGTACAGAAATGGCTCAAAAAGAGTCTAGAAGATGCTCATTTGAC 345

QY      41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
DB      346 ATCCAGTGCATCTCTTTCTTAAGGGAATCAGAGGCAATGAGCCCGCTATATCTCAACTCAA 405

QY      61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB      406 GAAGACTGCATTAATTTCTTGCTGTTCAACAAAACATATCAGGGGCAACAGCATGTAC 465

QY      81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysPheLeuPheCys 100
DB      466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCACTGCTACCTATTTTCTGT 525

QY      101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgleille 120
DB      526 CCCAACGAGGAGCCTGCTCCATTGAAACCCAGCAAGGAGCTTATGAGTTACAGGTAATT 585

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RESULT 3
AAF44268
ID AAF44268 standard; cDNA; 2284 BP.
XX
AC AAF44268;
XX
DT 02-APR-2001 (first entry)
XX

```

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QY      121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB      586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAGAGTTACCCAGGAAGATTCT 645

QY      141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB      646 CTCCTACATGGCCAAATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705

QY      161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB      706 TCAAAAGCCACCAGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

QY      181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB      766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCACGCTCCTCTTTATAGGAA 825

QY      201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220
DB      826 AAAGGCCATTTCTCAGAGTTTCACAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCC 895

QY      221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB      896 GAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCT 945

QY      241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB      946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCACTGACACCTTCTGGGACTTC 1005

QY      261 GlnProGlnLeuAlaThrThrAlaProValThrThrValThrSerGlnProProThr 280
DB      1006 CAGCCACAGCTGGCCACACACAGCTCCACCTGTAACCACTGTCTCAGCTCCACG 1065

QY      281 ThrLeuLeuSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB      1066 ACCCTCATTTCTCAGATTTTACACGGCTGGGCTTACTCTCCAGCAATGGCTACAA 1125

QY      301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB      1126 GCAGTTCTGACTTACCACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAAC 1185

QY      321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
DB      1186 CCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCTTCTGCA 1245

QY      341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
DB      1246 CTTTCTATGTCAATGTGAGTCTTCCACTATGAATAAACTGCTTCTCGGAAGGTAGG 1305

QY      361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB      1306 GAGGCCAGTCCAGGCAGTTCTCTCCAGGCAGTGTTCAGAAATACAGTACGCCCTTCCA 1365

QY      381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValleilleGly 400
DB      1366 TTGAAAAATGGCTTTCTTATCGGTCCTGCTCTTTGGTGTCTGTCTGCTGTAGAGC 1425

QY      401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
DB      1426 CTCGTCTCTCGGGTAGAATCCTTTGGGAATCACTCCGCGAGAAACGTTTCTCAAGACTG 1485

QY      421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB      1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

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DE Human PRO361 nucleotide sequence SEQ ID NO:514.

XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;

KW cancer; chromosomal mapping; gene mapping; tissue typing;

KW diagnostic assay; ss.

XX Homo sapiens.

OS

XX WO200073454-A1.

FN

XX 07-DEC-2000.

XX

XX 30-MAR-2000; 2000WO-US008439.

XX

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 17-AUG-1999; 99US-0149396P.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 08-OCT-1999; 99US-0158663P.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006894.

PR 20-MAR-2000; 2000WO-US007377.

XX

PA (GETH ) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PU;

PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;

PI Zhang Z;

XX

XX WPI; 2001-032160/04.

DR P-PSDB; AAB65299.

XX

PT PRO polynucleotides used to produce polypeptides used to target bioactive

PT molecules such as toxins, radiolabels or antibodies, to specific cells,

PT to cause targeted cell death.

XX

PS Claim 2; Fig 327; 935pp; English.

XX

CC The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can

CC be used for targeted delivery of bioactive molecules, such as toxins,

CC radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA and

CC DNA. They may also be used to produce transgenic animals which are used

CC to develop and screen therapeutically useful reagents. The PRO nucleotide

CC and protein sequence can be used for tissue typing and in treating

CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to

CC AAF44470 represent PCR primers and hybridisation probes used in the

CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to

CC AAB65300 represent human PRO polynucleotide and protein sequences given

CC in the exemplification of the present invention

XX

XX Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.02e-141 Length: 2284

Score: 2211.00 Matches: 431

Percent Similarity: 100.00% Conservatism: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-10-735-014-83 (1-431) x AAF44268 (1-2284)

Qy 1 MetPheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20

Db |||||

Qy 226 ATGTTCTTCGGGGGAGAGGAGCTTGACATTGCTTAATAATTGCTTCTCTGACA 285

Db |||||

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40

Db |||||

Qy 286 CTAAGGCTGTCTGCTAGTCAGAAATTCCTCAAAAGAGTCTAGAAGATGTTGTCATTGAC 345

Db |||||

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db |||||

Qy 346 ATCCAGTCATCTCTTCTTAAGGAATCAGAGCAATGAGCCGCTATATATCTTCACTCAA 405

Db |||||

Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80

Db |||||

Qy 406 GAAGACTGCATTAATTCTTCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465

Db |||||

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

Db |||||

Qy 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCCACTGCTACCTATTTCCTGT 525

Db |||||

Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIle 120

Db |||||

Qy 526 CCAACGAGGAGAGCTGTCATTTGAACACCAAGCAAAAGACTTATGATTCAGGATTAATT 585

Db |||||

Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

Db |||||

Qy 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCAAGATTTACCCAGGAAGATTCT 645

Db |||||

Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160

Db |||||

Qy 646 CTCTTACATGCCCAATTTTCCAAAGCAGTCACTCCCTAGCCCATCATCAACAGATTAAT 705

Db |||||

Qy 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180

Db |||||

Qy 706 TCAAGGCCACCCAGATATCTCATGGAGAGACACACTTCTCAGAAAGTTTGGATCCTCAGAT 765

Db |||||

Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200

Db |||||

Qy 766 CACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCCGAGCTCCTTGCTTATAAGGAA 825

Db |||||

Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220

Db |||||

Qy 826 AAGAGCCATTTCTCAGAGTTTCCCAATTTTCTCTGATCAAGAAATAGTCACTGCTGCTCCT 885

Db |||||

Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240

Db |||||

Qy 886 GAAATGTGATGGCTCCAGCTACGGTGGAGTGTGCTTCTCCACATACACCTCCGGCT 945

Db |||||

Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260

Db |||||

Qy 946 ACTCCAAAGCCGCGCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Db |||||

Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280

Db |||||

Qy 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCTTCCACCG 1065

Db |||||

Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300

Db |||||

Qy 1066 ACCCTCATTTCTACAGTTTTCACGGGCTCGGCTACACTCCAGCAATGGCTACAACA 1125

Db |||||

Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320

Db |||||

Qy 1126 GCAGTTCTGACTACCACTTTTCAGGCACTTACGAGCTCGAAGAGCAGCTTAGAAGCAATA 1185

Db |||||

QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 |||||  
 Db 1186 CCGTTTACAGAAATCTCCAACTTAACCTTGAACACAGGGAATGCTGTATAACCTACTGCA 1245  
 |||||  
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 |||||  
 Db 1246 CTTTCTATGTCAATGTGAGAGCTTCCATATGAATAAACTGCTTCCCTGGGAAGGTAGG 1305  
 |||||  
 QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 |||||  
 Db 1306 GAGGCCAGTCCAGGCAGTCTCCAGGAGGAGTGTCCAGAAATCAGTACGGCCTTCCA 1365  
 |||||  
 QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 |||||  
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCGGTGATAGC 1425  
 |||||  
 QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
 |||||  
 Db 1426 CTCGTCCTCTGGGTAGAATCCTTTCCGGAATCACTCCGAGAAACGTTTACTCAAGACTG 1485  
 |||||  
 QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 |||||  
 Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518  
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 RESULT 4  
 ACA64519  
 ID ACA64519 standard; cDNA; 2284 BP.  
 XX  
 AC ACA64519;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO361 cDNA.  
 XX  
 KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;  
 KW virucide; hepatotropic; antinflammatory; neuroprotective; gene therapy;  
 KW PRO; pharmaceutical; diagnostic; biosensor; bioeffector; malignancy;  
 KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
 KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
 KW drug screening; gene; ss.  
 XX  
 XX Homo sapiens:  
 XX  
 OS US2003003531-A1.  
 PN  
 XX  
 XX 02-JAN-2003.  
 PD  
 XX  
 PF 19-NOV-2001; 2001US-00989734.  
 XX  
 PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-0088212P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088655P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088738P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088826P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088861P.  
 PR 11-JUN-1998; 98US-0088876P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089440P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 17-JUN-1998; 98US-0089538P.  
 PR 17-JUN-1998; 98US-0089598P.  
 PR 17-JUN-1998; 98US-0089599P.  
 PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089907P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941932.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX



PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard J, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Pan J, Padoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI; 2003-352829/33.

DR P-PSDB; ABU72590.

XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or

PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
 PT disease.

XX Claim 1; Fig 327; 663pp; English.

CC The invention describes a new isolated nucleic acid molecule comprising  
 CC the full length coding sequence of the DNA deposited with the American  
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,  
 CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA  
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
 CC are particularly useful for detecting or treating e.g. malignancies or  
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
 CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
 CC disease in mammals. The PRO polypeptides are useful in drug screening,  
 CC particularly as targets for therapeutic intervention in these diseases,  
 CC and in the diagnostic determination of the presence of these diseases.  
 CC The PRO polypeptides are also useful as molecular weight markers, or for  
 CC chromosome identification. The PRO genes are useful as hybridisation  
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
 CC The PRO genes may also be used in gene therapy, particularly for  
 CC replacing a defective gene. This sequence encodes a novel human secreted  
 CC and transmembrane PRO polypeptide

XX SQ Sequence 2284 BP: 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ACA64519 (1-2284)

Qy 1 MetPheGlyGlyGlyGlySerLeuThrThrThrLeuValIleCysPheLeuThr 20  
 Db 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTCTGACA 285  
 Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuIleCysLeuValIleAsp 40  
 Db 286 CTAAAGGCTGCTGCTAGTCAGAAATGGCCCTCAAAAGAGTCTAGAGATGTTGTCATTGAC 345  
 Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrSerThrGln 60  
 Db 346 ATCCAGTCATCTCTTCTTAAGGGATCAGAGCAATGAGCCCGTATATCTCACTCAA 405  
 Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGCATTAATCTTGCTGTCAACAAAAACATATCAGGGGCAAAAGCATGTAAC 465  
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPheCys 100  
 Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTATTTTCTGT 525  
 Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgIleIle 120  
 Db 526 CCCAACGAGGAGGCTGTCCTTGAACACGAAAGAGCACTTATGAGTTACAGATTAAT 585  
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

Db 586 ACAGATTTCATCTTTCACCAAGAAATTTCCCAAGCAAGAGTTACCCAGGAAGATTCT 645  
 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 Db 646 CTCTTACATGGCCAAATTTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
 Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAAGCCCAACCATATCTCATGGAGAGACACACTTTCTCAGAAGATTGGATCCTCAGAT 765  
 Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200  
 Db 766 CACCTGGAGAAACATTTTAAAGATGGATGAAGCAAGTCCCGAGCTCTTGTCTTATAAGGAA 825  
 Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220  
 Db 826 AAAGGCCATTTCTCAGAGTTTCACTTTCTCTGATCAAGAAATAGTCTATCTGCTGCT 885  
 Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 Db 886 GAAAATGTGAGTGGCTCCAGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGCT 945  
 Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCCAAAGCCCGCCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
 Qy 261 GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr 280  
 Db 1006 CAGCCACAGTGGCCACACAGCTCCACCTGTAACTGTAACCTTCTCAGCTCTCCACG 1065  
 Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGGGCTACACTCCCAAGCAATGGCTTACAACA 1125  
 Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGCAGCTTAGAAACCATTA 1185  
 Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 Db 1186 CCGTTTACAGAAATCTCCAACTTAACCTTGAACACAGGGAATGTATTAACCTTACTGCA 1245  
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 Db 1246 CTTTCTATGTCAAATGTGAGTCTTCCACTATGATAATAAACTGCTTCTCTGGGAAGTAGG 1305  
 Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 Db 1306 GAGGCCAGTCCAGCAGTCTCTCCAGGGCAGTGTCCAGAAATCAGTACGGCTTCCA 1365  
 Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTGTGTCCTGTCCTGTCGTATAGGC 1425  
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
 Db 1426 CTCGCTCTCTCGGTGAGATCTTCCGAATCACTCCGAGAAACGTTACTCAAGACTG 1485  
 Qy 421 AspTyrIleLeuAsnGlyIleTyrValAspIle 431  
 Db 1486 GATTATTGATCAATGGATCTATGTGGACATC 1518  
 RESULT 5  
 ABX96832  
 ID ABX96832 standard; cDNA; 2284 BP.  
 XX AC  
 XX ABX96832;  
 XX AC  
 XX 15-MAY-2003 (first entry)  
 XX DT  
 XX Human cDNA encoding secreted/transmembrane protein PRO361.  
 XX DE  
 XX Human; ss; gene; PRO; secreted protein; transmembrane protein;



Cornelia de Lange syndrome; gene therapy; immune disorder;  
 inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;  
 diabetic complication.

Homo sapiens.

US2002173463-A1.

21-NOV-2002.

31-AUG-2001; 2001US-00944944.

03-DEC-1997; 97US-0067411P.

11-DEC-1997; 97US-0069278P.

11-DEC-1997; 97US-0069334P.

11-DEC-1997; 97US-0069335P.

12-DEC-1997; 97US-0069425P.

16-DEC-1997; 97US-0069694P.

16-DEC-1997; 97US-0069696P.

16-DEC-1997; 97US-0069702P.

17-DEC-1997; 97US-0069870P.

17-DEC-1997; 97US-0069873P.

18-DEC-1997; 97US-0068017P.

05-JAN-1998; 98US-0070440P.

09-FEB-1998; 98US-0074086P.

09-FEB-1998; 98US-0074092P.

25-FEB-1998; 98US-0075945P.

16-SEP-1998; 98WO-US019330.

01-DEC-1998; 98WO-US025108.

16-DEC-1998; 98US-0112850P.

22-DEC-1998; 98US-0113296P.

02-JUN-1999; 99WO-US012252.

28-JUL-1999; 99US-0146222P.

15-SEP-1999; 99WO-US021090.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

16-DEC-1999; 99WO-US030095.

11-FEB-2000; 2000WO-US003565.

22-FEB-2000; 2000WO-US004414.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

28-JUL-2000; 2000WO-US020710.

01-DEC-2000; 2000WO-US032678.

CC heterologous amino acid sequence and an antibody which specifically binds  
 CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,  
 CC in chromosome and gene mapping, in generating sense and antisense RNA or  
 CC DNA, in generating transgenic or knock-out animals which can be used in  
 CC the development and screening of therapeutically useful reagents, and in  
 CC gene therapy. The polypeptides may be used as molecular weight markers  
 CC for protein electrophoresis purposes. The PRO polypeptides and nucleic  
 CC acids may also be used for chromosome identification, and tissue typing.  
 CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange  
 CC syndrome. Other PRO proteins are variously implicated in immune  
 CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac  
 CC injury, infertility, birth defects, premature aging, cardiac injury,  
 CC AIDS, cancer and diabetic complications. The present sequence encodes a  
 CC PRO protein  
 XX

SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX96832 (1-2284)

QY 1 MetPheGlyGlyGlyGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20  
 Db 226 ATGTTCTTCGGGGGAGAGGGAGCTTGACTTACATTTTGTATTAATTTGCTTCTGACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40  
 Db 286 CTAAGGCTGTCTGCTAGTACAGAAATTCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345  
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
 Db 346 ATCCAGTCTATCTCTTCTTAAGGGAAATCAGAGCAATGAGCCCGTATATATCTCAACTCAA 405  
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGCATTAATCTTCTGTTCAACAAAACATATCAGGGGACAAAGCATGTAAC 465  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGT 525  
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 Db 526 CCCAACGAGGAGCCTGTCCATTGAACCCAGCAAAAGGACTTATGAGTTACAGGATAAT 585  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCAAGAGTATACCCGAGGAAGATTCT 645  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 Db 646 CTCCTACATGCCAATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
 QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAGCCGCCGATATCTCATGGAGAGACACACTTTCTCAGAAAGTTGGATCCTCAGAT 765  
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
 Db 766 CACTGGGAGAACTATTTAAGATGATGAAGCAAGTGGCCAGCTCTTCTTATAGGAA 825  
 QY 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
 Db 826 AAAGCCCATTTCTCAGAGTTTCAATTTTCTTGTATCAAGAAATAGCTCATCTGCTGCT 885  
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla 240

Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
 Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
 Hillan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
 WPI; 2003-311003/30.  
 P-PSDB; ABU64930.  
 New transmembrane polypeptides and polynucleotides useful for chromosome  
 identification, tissue typing, gene therapy, in chromosome and gene  
 mapping, or as molecular weight markers.  
 Claim 2; Fig 31; 172pp; English.  
 The invention relates to an isolated nucleic acid encoding a secreted/  
 transmembrane polypeptide (designated as PRO proteins). 15 PRO  
 polypeptides and their encoding polynucleotides are disclosed. Also  
 included are a vector comprising the PRO nucleic acid, a host cell  
 comprising the vector, a process for producing a PRO polypeptide (by  
 culturing the host cell under conditions for the expression of the PRO  
 polypeptide, and recovering the PRO polypeptide from the cell culture, an  
 isolated polypeptide having at least 80% amino acid sequence identity to  
 the PRO polypeptides, a chimaeric molecule comprising PRO fused to a

Db 886 GAAATGTGAGTGGCTCCACGACGTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945  
 Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGGACACCTTCTGGGACTTCC 1005  
 Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
 Db 1006 CAGCACAGCTGGCCACACAGCTCCACCTGTACCACTGTCACTTCTCAGCCTCCACAG 1065  
 Qy 281 ThrLeuLeSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 Db 1066 ACCCTCATTTCTACAGTTTTTACAGCGCTCGCGCTACACTCCAAGCAATGGCTACAACA 1125  
 Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 Db 1126 GCAGTTCTGACTACCACTTTCAGGCACCTACGAGCTCGAAAGGCACTTATGAAACCAT 1185  
 Qy 321 ProPheThrGluLeuSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 Db 1186 CCGTTACAGAAATCTCCAACTTAACTTTGACACAGGGAATGTATTAACCTTACTGCA 1245  
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 Db 1246 CTTTCTATGTCAAATGTGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGTAGG 1305  
 Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluLeuAsnGlnTyrGlyLeuPro 380  
 Db 1306 GAGGCCAGTCAGGAGTCTCTCCAGGAGTGTTCAGAAATCAGTACGGGCTTCCCA 1365  
 Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 Db 1366 TTGGAATAAGCTCTTATCGGTCCCTGCTCTTTGGTGCTTCTGCTGATAGGC 1425  
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420  
 Db 1426 CTCGTCTCTCTGGGTAGAACTCTTTCGGAATCACTCCGAGAAACGTTACTCAAGACTG 1485  
 Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 Db 1486 GATTATTGTCAATGGGATCTATGTGGACATC 1518  
 RESULT 6  
 ID ABX78486 standard; DNA; 2284 BP.  
 XX AC ABX78486;  
 XX DT 14-APR-2003 (first entry)  
 XX DE DNA encoding Novel human secreted protein PRO361.  
 XX KW Human; antiinflammatory; antiarteriosclerotic; cardiast; gynecological;  
 KW anti-HIV; cytosstatic; antidiabetic; BMP-agonist; BMP-Antagonist;  
 KW cytokine-agonist; cytokine-antagonist; gene-Therapy;  
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 KW infertility; birth defect; premature aging; AIDS; cancer;  
 KW diabetic complication; gene; ds.  
 XX OS Homo sapiens.  
 XX PN US2002150976-A1.  
 XX PD 17-OCT-2002.  
 XX PF 30-AUG-2001; 2001US-00943851.  
 XX PR 03-DEC-1997; 97US-0067411P.  
 PR 11-DEC-1997; 97US-0069278P.  
 PR 11-DEC-1997; 97US-0069334P.  
 PR 12-DEC-1997; 97US-0069335P.  
 PR 16-DEC-1997; 97US-0069425P.  
 PR 16-DEC-1997; 97US-0069694P.

PR 16-DEC-1997; 97US-0069696P.  
 PR 16-DEC-1997; 97US-0069702P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 17-DEC-1997; 97US-0069873P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 05-JAN-1998; 98US-0070440P.  
 PR 09-FEB-1998; 98US-0074086P.  
 PR 09-FEB-1998; 98US-0074092P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 16-DEC-1998; 98US-00216021.  
 PR 16-DEC-1998; 98US-0112850P.  
 PR 22-DEC-1998; 98US-00218517.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 03-MAR-1999; 99US-00254311.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 25-MAY-2001; 2001US-00866028.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WJ;  
 XX WPI; 2003-198285/19.  
 DR P-PSDB; ABUS8364.  
 XX New isolated PRO polypeptide and encoding nucleic acids, useful for the  
 PT diagnosis and treatment of disorders such as inflammatory disease,  
 PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic  
 PT complications.  
 XX Claim 2; Fig 31; 171pp; English.  
 XX The invention describes a novel isolated PRO polypeptide. The methods and  
 CC compositions of the present invention are useful for the diagnosis and  
 CC treatment of disorders such as inflammatory disease, organ failure,  
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature  
 CC aging, AIDS, cancer, diabetic complications and mutations in general.  
 CC This sequence encodes a novel human secreted PRO protein  
 XX SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. NO.: 1.02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-735-014-83 (1-431) x ABX78486 (1-2284)  
 Qy 1 MetPheGlyGlyGlyGlySerLeuThrThrThrLeuValIleIleCysPheLeuThr 20  
 Db 226 ATGTCTTCGGGGGAAGGAGGCTTACCTTGTATATATTTGCTTCTCTGACA 285  
 Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40

Db 286 CTAAGGCTGTCTGCTAGTCAGAAATTCCTCAAAAAGAGTCTAGAAGATGTTGTCAATGAC 345  
QY 41 IIEGINSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
Db 346 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGGCAATGAGCCGTATATATCTCAACTCA 405  
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCAATTAATCTTCTGCTGTTCAACAAAAACATATCATCAGGGACAAAGCATGTAA 465  
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysThrLysPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGCAACCACTGCTACCTATTTTCTGT 525  
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgIleIle 120  
Db 526 CCCAAGCAGAGCCCTGCTCCANTGAAACCCAGCAAGGACTTATGAGTTACAGGATAT 585  
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTCT 645  
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspThr 160  
Db 646 CTCCTACATGGCCAAATTTTCAAGCAGTCACCTCCCTAGCCCATCATCACACATAT 705  
QY 161 SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCARAAGCCACCGATATCTATCGAGAGACACACTTTCTCAGAAGTTGGATCCTCAGAT 765  
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaThrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA 825  
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885  
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGAGTGGCTCCACAGTACGCTGGAGTGTCTTCCACATACACACTCGGCT 945  
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
QY 261 GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTAAACCACTGTCTCAGCTCCCAAG 1065  
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTHACAGGCTGCGGTACACTCCAAGCAATGGCTCAACA 1125  
QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAGGAGGAGCTTAGAAACCAT 1185  
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACCTTAATCTTGAAACACAGGGAATGTGTATAACCTTACTG 1245  
QY 341 LeuSerMetSerAsnValGluSerSerThrThrMetAsnLysThrAlaSerThrGluGluV 360  
Db 1246 CTTTCTATGTCAATGTGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGTAGG 1305  
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnThrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGGAGTCTCTCCAGGCGAGTGTCCAGAAATCAGTACGGCCCTTCCA 1365  
QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400

Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGGTATAGGC 1425  
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTCTGGTGAATCCTTTCCGAATCACTCCGAGGAAAGCTTACTCAAGACTG 1485  
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518  
RESULT 7  
ABX77120  
ID ABX77120 standard; cDNA; 2284 BP.  
XX  
AC ABX77120;  
XX  
DT  
XX 04-APR-2003 (first entry)  
DE cDNA encoding human PRO361 protein.  
XX  
KW Gene; ss; human; antiinflammatory; antiarteriosclerotic; cardiant;  
anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;  
antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility;  
anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect;  
inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
premature aging; AIDS; cancer; diabetic complication.  
XX  
OS Homo sapiens.  
XX  
PN US2002142958-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 30-AUG-2001; 2001US-00943762.  
XX  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
Hillan KJ, Kljavin IJ, Napier WA, Roy MA, Tumas D, Wood WI;  
XX  
DR WPI; 2003-174140/17.  
DR P-PSDB; ABU57251.  
XX  
PT New secreted and transmembrane nucleic acids and polypeptides, designated  
as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
cardiac injury, infertility, birth defects, premature aging, AIDS, or  
cancer.  
XX  
PS Claim 2; Fig 31; 173pp; English.  
XX  
CC This invention relates to a nucleotide sequence encoding an isolated  
secreted and/or transmembrane protein. The nucleotide sequences of the  
invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti  
-infertility, anti-HIV, cytostatic and antidiabetic activities and may be

used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a nucleic acid sequence of the invention

XX Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1,02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX77120 (1-2284)

QY 1 MetPhePheGlyGlyGluGlySerLeuThrThrThrLeuValIleIleCysPheLeuThr 20  
 DB 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTTTACACTTTTGGTAATAATTGCTTCTGCACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40  
 DB 286 CTAAGGCTGTCTGCTAGTCAGAAATGCTCTCAAAAGAGCTAGAGAAATGTTGTCATTGAC 345  
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
 DB 346 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGCAATGAGCCGCTATATCTTCAACTCAA 405  
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 DB 406 GAAGACTGCATTAATTCCTGTGCTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 DB 466 TTGATGATCTCGACACTCGAANAACAGCTAGACACCAACTGCTACCTATTTTCTGT 525  
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 DB 526 CCCAACGAGGAAGCTGTCCATTGAACACGAGAAAGGACTTATGAGTTACAGGATAATT 585  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 DB 586 ACAGATTTTCCATCTTTGACGAGAAATTTGCCAAGCCCAAGAGTTACCCAGGAAGATTCT 645  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 DB 646 CTCTTACATGCCCAATTTTTCACAGCAGTCTCTCCCTAGCCCATCATCACAGATTAT 705  
 QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 DB 706 TCAAGCCCAACCGGATATCTCTGAGAGACACACTTTCTCAGAAAGTTGGATCCTCAGAT 765  
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
 DB 766 CACCTGGAGAAACTATTTAAGATGGATGAACCAAGTGCACAGCTCTTGGCTTATAAGGAA 825  
 QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
 DB 826 AAAGGCCAATTTCTCAGAGTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885  
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 DB 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCT 945  
 QY 241 ThrProLysProAlaThrLeuLeuProThrHisAlaSerValThrProSerGlyThrSer 260  
 DB 946 ACTCCAAAGCCCGCCACTTCTTACCCCAACCAATGCTTTCAGTGACACCTTCTGGGACATTC 1005

QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
 DB 1006 CAGCCACAGCTGGCCACCACAGCTCCACTGTAACTGTAACCACTGCTCACTTCTCAGCCTCCACG 1065  
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 DB 1066 ACCTCATTTCTACAGTTTTTACACGGCTGCGGCTACACTCCCAAGCAATGGCTTACAACA 1125  
 QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 DB 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTTACGAGCTCGAAAGCAGCTTAGAAACCAT 1185  
 QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 DB 1186 CCGTTTACAGAAATCTCCAATTAACCTTGAACACACAGGGAATGTGTATTAACCTTACTGCA 1245  
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 DB 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCGGAAGGTAGG 1305  
 QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 DB 1306 GAGGCCAGTCCAGCAGTCTCTCCAGGCGAGTTCAGAAATCAGTACGGCTTCCA 1365  
 QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 DB 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTGTCTTCTGGTATAGGC 1425  
 QY 401 LeuValLeuGlyArgIleLeuSerGluSerLeuArgLysArgLysArgTyrSerArgLeu 420  
 DB 1426 CTCGTCCTCTGGGTAGAACTCTTTCGGAATCACTCCGCAAGAAACGTTACTCAAGACTG 1485  
 QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 DB 1486 GATTATTGATCAATGGATCTATGTGGACATC 1518  
 RESULT 8  
 ABX80978  
 ID ABX80978 standard; cDNA; 2284 BP.  
 XX  
 AC ABX80978;  
 XX  
 XX 22-APR-2003 (first entry)  
 XX  
 DE Human secreted/transmembrane protein cDNA, #182.  
 XX  
 KW Human; gene, ss; PRO; secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;  
 KW tumour-associated antigenic target; TAT; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
 XX Homo sapiens.  
 XX US2003027162-A1.  
 FN  
 XX  
 XX 06-FEB-2003.  
 PD  
 XX  
 XX 15-NOV-2001; 2001US-00997428.  
 PF  
 XX 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
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PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
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PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
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PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
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PR 10-JUN-1998; 98US-0088742P.  
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PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
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PR 17-JUN-1998; 98US-0089532P.  
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PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089948P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
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PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090542P.  
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PR 25-JUN-1998; 98US-0090676P.  
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PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
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PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
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PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
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PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095923P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 17-AUG-1998; 98US-0096577P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
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PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096953P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
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PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 98WO-US005028.  
PR 12-MAR-1999; 98US-0123957P.  
PR 02-JUN-1999; 98WO-US012252.  
PR 23-JUN-1999; 98US-0141037P.  
PR 07-JUL-1999; 98US-0143048P.  
PR 20-JUL-1999; 98US-0144758P.  
PR 26-JUL-1999; 98US-0145698P.  
PR 28-JUL-1999; 98US-0146222P.  
PR 17-AUG-1999; 98US-0149396P.  
PR 15-SEP-1999; 98WO-US021090.  
PR 15-SEP-1999; 98WO-US021547.  
PR 08-OCT-1999; 98US-0158663P.  
PR 30-NOV-1999; 98WO-US028313.  
PR 01-DEC-1999; 98WO-US028301.  
PR 01-DEC-1999; 98WO-US028634.  
PR 16-DEC-1999; 98WO-US030095.  
PR 20-DEC-1999; 98WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.

Alignment Scores:  
 Pred. No.: 1.02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX80978 (1-2284)

QY 1 MetPheGlyGlyGlyGlySerLeuThrThrLeuValIleCysPheLeuThr 20  
 DB 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACCTTGGTAATTTGCTCTGACA 285

QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40  
 DB 286 CTAAGGCTGTCTGCTAGTACAGAAATTCCTCAAAAGAGCTAGAAAGATGTTGTCATTGAC 345

QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
 DB 346 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGGCATAGCCCGTATATACCTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 DB 406 GAAGACTGCATTAATTTCTGTCTTCAACAAAACATATCAGGGGCAAGCATGTAAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 DB 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCCAACTGCTACTATTTTCTGT 525

QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 DB 526 CCCAACGAGGAGCCTGTCCATTGAAACCAAGAAAGGACTTATGAGTTACAGGATTAAT 585

QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 DB 586 ACAGATTTTCCATCTTTGACCCAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCT 645

QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 DB 646 CTCCTACATGGCCAAATTTTCAAGAGCAGTCACTCCCTTAGCCCATCATCACAGATTAT 705

QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 DB 706 TCAAGCCCAACCGATATCTCATGAGAGACACACTTTCTCAGAAAGTTTGGATCTCTCAGAT 765

QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
 DB 766 CACCTGGAGAAACATTTTAAGATGGATGAGCAAGTGCCAGCTCTCTGCTTATAAGGAA 825

QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
 DB 826 AAAGGCCATTTCTCAGAGTTCAAAATTTTCTCTGATCAAGAAATAGTCTCATCTGCTGCT 885

QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 DB 886 GAAATGTGAGTGGCTCCCGAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCT 945

QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 DB 946 ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
 DB 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAACTGTAACCACTGCTCACTTCTCAGCTCCCAAG 1065

QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 DB 1066 ACCCTCATTTCTACAGTTTTCACACGGGCTGCGGCTACATCTCCAAGCAATGGCTTACAA 1125

QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 DB 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTTCAGGACTCGAAGGCGAGCTTAGAAACCAT 1185

QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 DB 1186 CCGTTTACAGAAATCTCCAACTTAACTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245

QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360  
 DB 1246 CTTTCTATGTCAAATGGAGTCTTCCACTATGAATAAACTGCTTCTCGGAAGGTAGG 1305

QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 DB 1306 GAGGCCAGTCCAGGCAGTCTCTCCAGGCGAGTTCACAGAAATCAGTACGGCTTCCA 1365

QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 DB 1366 TTTGAAATAATGGCTTCTTATCGGCTCCCTGCTCTTTGGTGTCTCTGTTCTCTGGTATAGG 1425

QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
 DB 1426 CTGCTCTCTCGGTAGATCTTTTCGAAATCACTCCGAGGAACGTTTACTCAAGACTG 1485

QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 DB 1486 GATTATTGATCAATGGATCTATGTGACATC 1518

RESULT 9  
 ACD44487  
 ID ACD44487 standard; cDNA; 2284 BP.  
 XX AC ACD44487;  
 XX AC ACD44487;  
 DT 10-SEP-2003 (first entry)  
 DE cDNA encoding human PRO361 polypeptide.  
 DE Human; PRO polypeptide; secreted protein; transmembrane protein;  
 KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
 KW gene therapy; gene; ss.  
 XX Homo sapiens.  
 XX OS  
 XX US2002127576-A1.  
 PN 12-SEP-2002.  
 PD 14-NOV-2001; 2001US-00991073.  
 PF 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.

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PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
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PR 10-JUN-1998; 98US-0088734P.
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PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX WPI; 2003-340824/32.
DR P-PSDB; ABO26036.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
XX Claim 2; Fig 327; 661pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipdbEntry.html
XX
SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.02e-141 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ACD44487 (1-2284)
QY 1 MetPhePheGlyGlyGlySerLeuThrTyThrLeuValIleIleCysPheLeuThr 20
pb 226 ATGTTCTTCGGGGGAGAGGGAGCTTGACTTTGCTAATTAATTTGCTCTTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
Db 286 CTAGGCTGCTGCTAGTACAGATTGCTCTCAAAAGAGCTCAGAGAGTGTCTCATTCAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyThrSerThrGln 60
```



Db 346 ATCCAGTCATCTCTTCTTAAGGAATCAGAGCAATGAGCCGTATATACCTCAACTCAA 405  
Qy 61 GluAspCysIleAsnSerCysCysSerThrIysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTAATTTCTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAANAACAGCTAGACAACTGCTACTATTTTCTGT 525  
Qy 101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAACGAGGAGCGCTGCTCAATGAAACCCAGAAAGGACTTATGAGTTACAGATAATT 585  
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGlnLeuProGlnLysSer 140  
Db 586 ACAGATTTTCCATCTTTCACCAAGAAATTTGCCAAGCCAGAGTTTACCCAGGAGATTC 645  
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCTTACATGGCAATTTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
Qy 161 SerIysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAGCCACCGCATATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACATATTTAAGATGATGAAGCAAGTGCCTGCTTGTATTAAGGAA 825  
Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGCCCATTTCTCAGAGTTTCAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885  
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla 240  
Db 886 GAAATGTGAGTGGCTCCAGTCCAGTACGGTGGCAGTTGCTTCCACATACCACTCGGCT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCAAAGCCCGCCACCTTCTACCAACCAATGCTTCAGTGACACCTTCTGGGACTTC 1005  
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTACCACTGTCACTTCTCAGCCTCCACG 1065  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCAATTTCTACAGTTTTCACACGGGCTCGGCTACACTCCAAGCAATGGCTACAACA 1125  
Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 CGAGTTCTGACTACCACTTTCAGCCACTCAGGACTCGAAAGGAGCTTAGAAACCATTA 1185  
Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACTTAACTTTGACACAGGAGATGTATACCCCTACTGCA 1245  
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGTAGG 1305  
Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluLysAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGCCAGTCCAGGAGTCTTCCAGGGCAGTGTTCAGAAATACAGTACGGCTTCCA 1365  
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuLeuValIleGly 400  
Db 1366 TTTGAAAAATGGCTTCTTATCGGTCCCTGCTCTTTTGGTGCTGCTTCTGCTGATAGGC 1425  
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTCTGGGTAGAATCCTTTCCGAATCACTCCGAGAAACGTTACTCAAGACTG 1485

Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518  
RESULT 10  
ABX75951  
ID ABX75951 standard; cDNA; 2284 BP.  
XX AC ABX75951;  
XX DT 31-MAR-2003 (first entry)  
XX DE Human cDNA encoding secreted/transmembrane protein, PRO361.  
XX KW Human; ss; gene; PRO; antiinflammatory; antiarteriosclerotic; cardiac;  
KW synecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease;  
KW organ failure; atherosclerosis; cardiac injury; infertility;  
KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;  
KW cancer; diabetic complication.  
XX OS Homo sapiens.  
XX PN US2002132981-A1.  
XX PD 19-SEP-2002.  
XX PF 30-AUG-2001; 2001US-00944396.  
XX PR 03-DEC-1997; 97US-0067411P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 16-DEC-1997; 97US-0069696P.  
PR 16-DEC-1997; 97US-0069702P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 17-DEC-1997; 97US-0069873P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 05-JAN-1998; 98US-0070440P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 12-DEC-1998; 98US-0112850P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 28-JUL-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX PA (GETH ) GENENTECH INC.  
XX PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX WPI; 2003-147446/14.  
DR P-PSDB; ABUS6315.  
DR



XX New isolated PRO polypeptide and encoding nucleic acids, useful for the  
 PT diagnosis and treatment of disorders such as inflammatory disease,  
 PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic  
 PT complications.

XX Claim 2; Fig 31; 171pp; English.

XX The invention relates to an isolated PRO polypeptide having at least 80%  
 CC amino acid sequence identity to and scoring at least 80% positives when  
 CC compared to any of 15 fully defined sequences of 235-954 amino acids,  
 CC given in the specification. Also included are: (1) an isolated PRO  
 CC nucleic acid having at least 80% nucleic acid sequence identity to a  
 CC nucleotide sequence that encodes PRO or its extracellular domain, and  
 CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,  
 CC given in the specification and deposited under ATCC accession number  
 CC 209526, 209508, 209524, 209528, 209530, 209523, 209532, 209531,  
 CC 209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector  
 CC comprising the PRO nucleic acid; (3) a host cell comprising the vector;  
 CC (4) producing PRO polypeptides, comprising culturing the cell for  
 CC expression of the PRO polypeptide and recovering the PRO polypeptide from  
 CC the cell culture; (5) a chimeric molecule comprising PRO fused to a  
 CC heterologous amino acid sequence; and (6) an anti-PRP antibody. The  
 CC methods and compositions are useful for the diagnosis and treatment of  
 CC disorders such as inflammatory disease, organ failure, atherosclerosis,  
 CC cardiac injury, infertility, birth defects, premature aging, AIDS  
 CC (acquired immunodeficiency syndrome), cancer, diabetic complications and  
 CC mutations in general. The present sequence is a cDNA encoding a PRO  
 CC polypeptide

XX SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 1-02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX75951 (1-2284)

QY 1 MetPheGlyGlyGlySerLeuThrThrLeuValleileCysPheLeuThr 20  
 Db 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTTGGTAATTTGCTTCTGACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnSerCysLeuLysLysSerLeuGluAspValleileasp 40  
 Db 286 CTAAGGCTCTGCTAGTACAGAAATTCCTCAAAAAGAGTCTAGAAGATGTTGCTATTGAC 345  
 QY 41 IleGlnSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
 Db 346 ATCCAGTCACTCTTTCTAAGGGAATCAGAGCAATGAGCCCGTATATACCTCAACTCA 405  
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGCAATTAATCTTCTGCTTCAACAAAAACATATCAGGGACCAAGCATGTAC 465  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGT 525  
 QY 101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIlelle 120  
 Db 526 CCCACGAGAGACCTGCTCCATTTGAACACCAAGAGGACTTATGAGTTACAGGATAAT 585  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 Db 586 ACAGATTTTCCATCTTTGACGAGAAATTTGCCAGCCAGAGATTACCCAGGAGATCT 645  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 Db 646 CTCTTACATGGCCAAATTTTACAAAGCAGTCACTCCCTAGGCCATCATCACACAGATTAT 705

QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAAGCCACCACCATATCTCATGGAGACACACATTTCTCAGAGATTGTCATCTCAGAT 765  
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
 Db 766 CACCTGGAGAAACTATTTAAGATGATGAAGCAAGTCCACCTCTTCTGCTTATAGGAA 825  
 QY 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGlnIleAlaHisLeuLeuPro 220  
 Db 826 AAAGGCCATCTCAGAGTTTCACATTTTCTCTGATCAGAAATAGCTCATCTGTCCT 885  
 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 Db 886 GAAATGTGAGTGGCTCCACGCTACGGTGGCAGTTGCTTCTCCACATACACACCTCGGCT 945  
 QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTTCAGTGACACCTTCTGGGACTTCC 1005  
 QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
 Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGPAACACTGTCTCTCAGGCTCCACG 1065  
 QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 Db 1066 ACCCTCATTTCTACAGATTTTACACGGCTGGGCTACACTCCAAAGCAATGCTCAACA 1125  
 QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 Db 1126 GCAGTTCTGACTTACCACCTTTTCCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAAC 1185  
 QY 321 ProPheThrGluIleSerAsnLeuThrLeuLeuThrGlyAsnValTyrAsnProThrAla 340  
 Db 1186 CCGTTTACAGAAATCTCCAACCTTAACACAGGGAATGTGTATACCTTACTGCA 1245  
 QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGTAG 1305  
 QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 Db 1306 GAGGCGAGTCCAGGCAGTTCCTCCAGGCGCAGTGTTCAGAAAAATCAGTACGCGCTTCA 1365  
 QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValleileGly 400  
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTTTTGGTGTCTCTTCTGCTGTAGGC 1425  
 QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
 Db 1426 CTCGTCCTCTGGGTAGAAATCTTTCCGAATCACTCCGAGAAACAGTTACTCAAGACTG 1485  
 QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 Db 1486 GATTATTGATCAATGGGATCTATGTGACATC 1518

## RESULT 11

ABX89662

ID ABX89662 standard; cDNA; 2284 BP.

XX AC ABX89662;

XX DT 28-APR-2003 (first entry)

XX DE cDNA encoding novel secreted and transmembrane protein PRO361.

XX KW Secreted and transmembrane polypeptide; PRO; tissue typing; gene therapy;

XX KW transgenic; knockout animal; inflammatory disease; organ failure;

XX KW atherosclerosis; cardiac injury; infertility; birth defect;

XX KW premature aging; acquired immunodeficiency syndrome; AIDS; cancer;

XX KW diabetic complication; immune system disorder; proteoglycan release;

XX KW sports-related joint problem; human; articular cartilage defect;

osteoarthritis; rheumatoid arthritis;  
 vascular endothelial cell growth factor stimulated proliferation;  
 endothelial cell growth; VEGF stimulated proliferation; Gene; ss.  
 OS Homo sapiens.  
 PN US2002168715-A1.  
 XX 14-NOV-2002.  
 PD 31-AUG-2001; 2001US-00944896.  
 PF 03-DEC-1997; 97US-0067411P.  
 PR 11-DEC-1997; 97US-0069278P.  
 PR 11-DEC-1997; 97US-0069334P.  
 PR 11-DEC-1997; 97US-0069335P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 16-DEC-1997; 97US-0069694P.  
 PR 16-DEC-1997; 97US-0069696P.  
 PR 16-DEC-1997; 97US-0069702P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 17-DEC-1997; 97US-0069873P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 05-JAN-1998; 98US-0070440P.  
 PR 09-FEB-1998; 98US-0074086P.  
 PR 09-FEB-1998; 98US-0074092P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 16-DEC-1998; 98US-00216021.  
 PR 16-DEC-1998; 98US-0112850P.  
 PR 22-DEC-1998; 98US-0021851P.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 03-MAR-1999; 99US-00254311.  
 PR 22-JUN-1999; 99WO-US012252.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US010442.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 25-MAY-2001; 2001US-00866028.  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
 XX WPI; 2003-275322/27.  
 DR P-PSDB; ABU60355.  
 DR Novel isolated PRO polypeptides e.g. PRO243, PRO299, PRO323, PRO327,  
 XX PRO344, and polynucleotides useful in the treatment of human disorders  
 PT related to immune system, and in gene therapy.  
 XX Claim 2; Fig 31; 173pp; English.  
 XX The invention describes an isolated secreted and transmembrane  
 CC polypeptide, designated as PRO polypeptide (I) having at least 80 %  
 CC identity to, a 379, 954, 737, 433, 422, 300, 243, 455, 694, 440, 598,  
 CC 250, 281, 431 or 235 amino acid sequence (SI), given in the  
 CC specification, SI lacking its associated signal peptide or extracellular  
 CC domain of SI with or without its associated signal peptide. (I) and the  
 CC polynucleotide (II) encoding it are useful in tissue typing and gene

CC therapy. (II) is also useful for generating transgenic animals or  
 CC knockout animals for the development and screening of therapeutically  
 CC useful reagents. PRO233 polypeptide is useful for treating inflammatory  
 CC disease, organ failure, atherosclerosis, cardiac injury, infertility,  
 CC birth defects, premature aging, acquired immunodeficiency syndrome  
 CC (AIDS), cancer and diabetic complications. The other PRO polypeptides  
 CC including PRO243, PRO299, PRO323, PRO327, PRO344, PRO354, PRO355,  
 CC PRO715, PRO353, PRO361 and PRO365 are useful for treating human disorders  
 CC involving the immune system. PRO241 is useful for stimulating release of  
 CC proteoglycans from cartilage, and thus for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis and rheumatoid  
 CC arthritis. (I) is also useful for inhibiting vascular endothelial cell  
 CC growth factor (VEGF) stimulated proliferation of endothelial cell growth.  
 CC This sequence encodes a novel human secreted and transmembrane protein  
 XX  
 SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1,02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX89662 (1-2284)

Qy 1 MetPheGlyGlyGluGlySerLeuThyThyThyLeuValIleleCysPheLeuThr 20  
 Db 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTGGTAATAAATTCCTTCCTGACA 285  
 Qy 21 LeuArgLeuSerAlaSerGlnAenCysLeuLysLysSerLeuGluAspValIleAsp 40  
 Db 286 CTAAGGCTGTCTGCTAGTCAGAAATTCCTCAAAAGAGCTAGAAAGTGTTCATTGAC 345  
 Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyThrSerThrGln 60  
 Db 346 ATCCAGTCATCTCTTCTAAGGGAATCAGAGCAATGAGCCCGTATATCTTCACTCAA 405  
 Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGTCATTAATTCCTGCTTCAACAAAACATATACAGGGGCAAAAGATGTAAC 465  
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaAtgGlnProAsnCysTyTrLeuPhePheCys 100  
 Db 466 TTGATGATCTTCGACTCGAAAAACAGCTAGACAAACCCACTGCTACCTATTTTCTGT 525  
 Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyArgIleIle 120  
 Db 526 CCCAACGAGGAGCCCTGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAAT 585  
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 Db 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCCAAGAGTATCCCCAGGAGATTC 645  
 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyTr 160  
 Db 646 CTCTTACATGGCCAAATTTTCAAGCAGTCATCTCCCTAGCCCATCATCACACAGATTAT 705  
 Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAGCCCAACCCGATATCTCATCGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765  
 Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyTrLysGlu 200  
 Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCTCTGCTTATTAAGGAA 825  
 Qy 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
 Db 826 AAGGCCATTCACAGAGTTCACAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885  
 Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240

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Db      886  GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945
Qy      241  ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db      946  ACTCAAAGCCGCCACCTTCTACCAACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
Qy      261  GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr 280
Db      1006  CAGCCACAGTGGCCACCACTCCACCTGTAAACCACTGTCACTTCTCAGCCCTCCACG 1065
Qy      281  ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Db      1066  ACCCTCATTTCTACAGTTTACACGGCTCGCGCTACACTCCCAAGCAATGGCTACACA 1125
Qy      301  AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db      1126  GCAGTTCTGACTACCACTTTTACAGGCACTTACGGACCTTACGGAGCGAGCTTAGAAACCA 1185
Qy      321  ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340
Db      1186  CCGTTTACAGAAATCTCCAACTTAACTTTGAACACACAGGGAATGTGTATAACCTACTGCA 1245
Qy      341  LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db      1246  CTTTCTATGTCAAAATGTGAGTCTTCACTATCAATGAATAAACTCTTCTGGGAGTAGG 1305
Qy      361  GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTrpGlyLeuPro 380
Db      1306  GAGGCCAGTCCAGGCAGTCTCTCCAGGGCAGTGTCCAGAAATCAGTACGGCCTTCCA 1365
Qy      381  PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db      1366  TTTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGTCTCTTCTGGTGATAGGC 1425
Qy      401  LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTrpSerArgLeu 420
Db      1426  CTGCTCTCTGGTGAATCTCTTTCGGAATCACTCCGAGGAACGTTACTCAAGACTG 1485
Qy      421  AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db      1486  GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 12
ABX79658
ID  ABX79658 standard; cDNA; 2284 BP.
XX
AC  ABX79658;
XX
DT  17-APR-2003 (first entry)
XX
DE  Human secreted/transmembrane protein cDNA, #182.
XX
KW  Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW  pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW  colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS  Homo sapiens.
XX
PN  US2002142961-A1.
XX
PD  03-OCT-2002.
XX
PF  19-NOV-2001; 2001US-00989721.
XX
PR  16-JUN-1997; 97US-0049787P.
PR  17-OCT-1997; 97US-0062250P.
PR  05-NOV-1997; 97WO-US020069.
PR  12-NOV-1997; 97US-0065186P.
PR  13-NOV-1997; 97US-0065311P.
PR  24-NOV-1997; 97US-0065770P.
PR  25-FEB-1998; 98US-0075945P.
PR  20-MAR-1998; 98US-0078910P.
PR  28-APR-1998; 98US-0083322P.
PR  07-MAY-1998; 98US-0084600P.
PR  28-MAY-1998; 98US-0087106P.
PR  02-JUN-1998; 98US-0087607P.
PR  02-JUN-1998; 98US-0087609P.
PR  02-JUN-1998; 98US-0087759P.
PR  03-JUN-1998; 98US-0087827P.
PR  04-JUN-1998; 98US-0088021P.
PR  04-JUN-1998; 98US-0088025P.
PR  04-JUN-1998; 98US-0088026P.
PR  04-JUN-1998; 98US-0088028P.
PR  04-JUN-1998; 98US-0088029P.
PR  04-JUN-1998; 98US-0088030P.
PR  04-JUN-1998; 98US-0088033P.
PR  04-JUN-1998; 98US-0088326P.
PR  05-JUN-1998; 98US-0088167P.
PR  05-JUN-1998; 98US-0088202P.
PR  05-JUN-1998; 98US-0088212P.
PR  05-JUN-1998; 98US-0088217P.
PR  09-JUN-1998; 98US-0088655P.
PR  10-JUN-1998; 98US-0088734P.
PR  10-JUN-1998; 98US-0088738P.
PR  10-JUN-1998; 98US-0088742P.
PR  10-JUN-1998; 98US-0088810P.
PR  10-JUN-1998; 98US-0088824P.
PR  10-JUN-1998; 98US-0088826P.
PR  11-JUN-1998; 98US-0088858P.
PR  11-JUN-1998; 98US-0088861P.
PR  11-JUN-1998; 98US-0088876P.
PR  12-JUN-1998; 98US-0089105P.
PR  16-JUN-1998; 98US-0089440P.
PR  16-JUN-1998; 98US-0089512P.
PR  16-JUN-1998; 98US-0089514P.
PR  17-JUN-1998; 98US-0089532P.
PR  17-JUN-1998; 98US-0089538P.
PR  17-JUN-1998; 98US-0089598P.
PR  17-JUN-1998; 98US-0089599P.
PR  17-JUN-1998; 98US-0089600P.
PR  17-JUN-1998; 98US-0089653P.
PR  18-JUN-1998; 98US-0089801P.
PR  18-JUN-1998; 98US-0089907P.
PR  18-JUN-1998; 98US-0089908P.
PR  16-SEP-1998; 98WO-US019330.
PR  17-SEP-1998; 98WO-US019437.
PR  07-OCT-1998; 98WO-US021141.
PR  01-DEC-1998; 98WO-US025108.
PR  05-JAN-1999; 99WO-US000106.
PR  08-MAR-1999; 99WO-US005028.
PR  02-JUN-1999; 99WO-US012252.
PR  15-SEP-1999; 99WO-US021090.
PR  15-SEP-1999; 99WO-US021547.
PR  30-NOV-1999; 99WO-US028313.
PR  01-DEC-1999; 99WO-US028301.
PR  01-DEC-1999; 99WO-US028634.
PR  16-DEC-1999; 99WO-US030095.
PR  20-DEC-1999; 99WO-US030911.
PR  05-JAN-2000; 2000WO-US000219.
PR  06-JAN-2000; 2000WO-US003376.
PR  11-FEB-2000; 2000WO-US003565.
PR  18-FEB-2000; 2000WO-US004341.
PR  22-FEB-2000; 2000WO-US004414.
PR  24-FEB-2000; 2000WO-US004914.
PR  24-FEB-2000; 2000WO-US005004.
PR  02-MAR-2000; 2000WO-US005841.
PR  10-MAR-2000; 2000WO-US006319.
PR  15-MAR-2000; 2000WO-US006884.
PR  20-MAR-2000; 2000WO-US007377.
PR  30-MAR-2000; 2000WO-US008439.
PR  15-MAY-2000; 2000WO-US013358.
PR  17-MAY-2000; 2000WO-US013705.
PR  22-MAY-2000; 2000WO-US014042.
PR  30-MAY-2000; 2000WO-US014941.
PR  02-JUN-2000; 2000WO-US015264.
PR  28-JUL-2000; 2000WO-US020710.
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PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI; 2003-155950/15.  
 DR P-FSDB; ABUS9045.  
 XX  
 PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 XX  
 PS Claim 2; Fig 327; 647pp; English.  
 XX  
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79250-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 SQ Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,02e-141 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-735-014-83 (1-431) x ABX79658 (1-2284)  
 QY 1 MetPheGlyGlyGluGlySerLeuThrThrLeuValIleCysPheLeuThr 20  
 DB 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACA 285  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40  
 DB 286 CTAAGGCTGCTGCTAGTCAGAAATTCCTCAAAAGAGCTCTAGAAGATGTTGTCATTGAC 345  
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrSerThrGln 60  
 DB 346 ATCCAGTCATCTCTTTCTTAAGGGAATCAGAGGCAATGAGGCCGATATATCTTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 DB 406 GAGACTGCAATTAATCTTCTGTTCAACAAAAAATATACAGGGGCAAGATGTATAC 465  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 DB 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCCACTTACCTATTTCTGT 525  
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 DB 526 CCCAACGAGGAAGCTGTCCATTGAACACGACCAAGAGACTTATGAGTTACAGGATAAT 585  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 DB 586 ACAGATTTTCACTTTTGACCAAAATTTGCCAAGCCAGAGATTACCCAGGAGATCT 645  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 DB 646 CTCTTACATGSCCAATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
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 DB 706 TCAAGCCCAACCGATATCTCATGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765  
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 DB 766 CACTGGAGAACTATTATTAAGATGGATGAAGCAAGTCCCGAGCTCTTGTCTTATAGGAA 825  
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 QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 DB 886 GAAATGTGAGTGGCTCCAGAGTCCAGTGGAGTGGCTTCTCCACATACACCTCCGCT 945  
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 DB 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCTCCACG 1065  
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XX AC ACA93679;  
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XX KW Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
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KW cytostatic; chromosome mapping; gene mapping; transgenic animal;  
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XX PN US2003022187-A1.  
XX PD 30-JAN-2003.  
XX PF 14-NOV-2001; 2001US-00993667.  
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PR	18-AUG-1998;	98US-0097022P.	Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValValIleasp	40
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PR	16-SEP-1998;	98US-0100634P.	Db	526	CCCAACGAGGAGCCTGTCCATTGAAACACAGCAAAAGGACTTATAGTTACAGGATATT	585
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PR	12-MAR-1999;	99US-0123957P.	Db	766	CACCTGGAGAAATATTATTAAGATCGATGAAGCAAGTCCAGCTCTCTGTCTTAAAGAA	825
PR	02-JUN-1999;	99WO-US012252.	Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
PR	27-JUL-1999;	99US-0141037P.	Db	826	AAAGGCCATTTCTCAGAGTTTCAAAATTTCTCTGTATCAAGAAATAGTCACTCTGCTCCT	885
PR	00-JUL-1999;	99US-0143048P.	Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
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PR	05-JAN-2000;	2000WO-US000219.	Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
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PR	18-FEB-2000;	2000WO-US004341.	Db	1126	GCAGTTCTGACTACCACTTTTCAGGCACCTTACGGGACTTCGAAAGGACGCTTAGAACCAT	1185
PR	22-FEB-2000;	2000WO-US004414.	Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
PR	24-FEB-2000;	2000WO-US004914.	Db	1186	CCGTTTACAGAAATCTCCAACTTAATTTGAAACACAGGGAATGTGTATATAACCTTACTGCA	1245
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KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; genes; ds.  
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XX  
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XX  
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SUMMARIES

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7	157	7.1	16562	4	US-09-949-016-13892
8	152	6.9	1297	4	US-09-976-594-950
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Alignment Scores: 1.97e-217 Length: 2284

ALIGNMENTS

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; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavini, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT FILING DATE: 2001-05-25  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 82  
; LENGTH: 2284  
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; ORGANISM: Homo Sapien  
US-09-866-028-82

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C 28	134	6.1	5163	4	US-09-588-995A-4	Sequence 4, Appli
C 29	134	6.1	5318	3	US-08-700-651-2	Sequence 2, Appli
C 30	134	6.1	5318	3	US-08-928-361B-3	Sequence 3, Appli
C 31	134	6.1	5318	4	US-09-588-995A-3	Sequence 3, Appli
C 32	133.5	6.0	867	4	US-09-216-393B-340	Sequence 340, App
C 33	133.5	6.0	867	4	US-09-216-393B-342	Sequence 342, App
C 34	133.5	6.0	1397	4	US-09-216-393B-343	Sequence 343, App
C 35	133.5	6.0	1397	4	US-09-216-393B-345	Sequence 345, App
C 36	133.5	6.0	1795	4	US-09-197-970B-5	Sequence 6, Appli
C 37	133	6.0	1671	4	US-09-614-221A-554	Sequence 554, App
C 38	132	6.0	2455	3	US-09-103-429A-1	Sequence 1, Appli
C 39	132	6.0	2455	4	US-09-294-663-1	Sequence 1, Appli
C 40	132	6.0	2821	3	US-09-103-429A-2	Sequence 2, Appli
C 41	132	6.0	2821	4	US-09-294-663-2	Sequence 2, Appli
C 42	132	6.0	5511	3	US-08-928-361B-2	Sequence 2, Appli
C 43	132	6.0	5511	4	US-09-588-995A-2	Sequence 2, Appli
C 44	132	6.0	7334	3	US-08-928-361B-1	Sequence 1, Appli
C 45	132	6.0	7334	4	US-09-588-995A-1	Sequence 1, Appli

Score: 2211.00 Matches: 431  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-735-014-83 (1-431) x US-09-866-028-82 (1-2284)

Qy 1 MetPheGlyGlyGluGlySerLeuThrThrThrLeuValIleIleCysPheLeuThr 20  
Db 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuIleYsSerLeuGluAspValIleLeasp 40  
Db 286 CTAAGGCTGTCTGCTAGTTCAGATTTGCTTCAAAAGAGTCTAGAGAGTTGTCTATGAC 345

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
Db 346 ATCCAGTTCATCTCTTCTAAGGGAATCAGAGCAATGAGCCGCTATATCTCAACTCAA 405

Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTAATCTTCTGTGTTCAACAAACATATATCAGGGGCAAAAGCATGTAAC 465

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAACAGTACAGCAACCCCACTGCTACCTATTTTCTGT 525

Qy 101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAACGAGGAAGCCTGTCCATTGAACACAGCAAAAGGACTTATGAGTTACAGGATAAT 585

Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnLysSer 140  
Db 586 ACAGATTTTCATCTTTGACCAAGAAATTTGCCAGCCCAAGAGTTACCCAGAGATTCCT 645

Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCITACATGGCCAAATTTTCACAGCAGTCTCTCCCTAGCCCATCATCACAGATTAT 705

Qy 161 SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAAGCCACCGCATATCTCATGGAGACACACTTTCTCAGAAAGTTGGATCCTCAGAT 765

Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACATATTTAAGATGATGAAGCAAGTGGCCAGCTCTTGTCTTAAGGAA 825

Qy 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCAATTTCTAGAGTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAAATGTGAGTGGCTCCAGCTACGCTGAGTGGCTTCTCCACATACCACTCGGCT 945

Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCAAAGCCGCCACCTCTTCAACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280  
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTACCTGTACCTTCTCAGCTTCCACG 1065

Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTCACAGGCTCGGCTACACTTCAAGCAATGGCTTACAACA 1125

Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 CGAGTTCGACTACCACTTTTCAGGACCTACGAGCTCGAAAGGAGCTTAGAAACATA 1185

Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340

Db 1186 CCGTTTACAGAAATCTCCAACCTTTGAACACAGGGAATGTATATAACCCCTACTGCA 1245

Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerThrGluGlyArg 360

Db 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCGGAAGGTAGG 1305

Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380

Db 1306 GAGGCCAGTCAGCAGCTTCTCCAGGGCAGTGTTCCAGAAATCAGTACGGCTTCCA 1365

Qy 381 PheGluLysThrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400

Db 1366 TTTGAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCGGTGATAGGC 1425

Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420

Db 1426 CTGCTCCTCGGTAGAACTCTTTCGGAATCACTCCGACGAAACGTTACTCAAGACTG 1485

Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1486 GATTATTGATCAATGGGATCTATGTGACATC 1518

RESULT 2  
US-09-944-457-82  
; Sequence 82, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavini, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440  
 ; PRIOR FILING DATE: January 5, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,086  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,092  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/075,945  
 ; PRIOR FILING DATE: February 25, 1998  
 ; PRIOR APPLICATION NUMBER: 60/112,850  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 60/113,296  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 60/146,222  
 ; PRIOR FILING DATE: July 28, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330  
 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/216,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. 6734288ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. 6734288ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 82  
 ; LENGTH: 2284  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-944-457-82

Alignment Scores:  
 Pred. No.: 1,976-217 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-735-014-83 (1-431) x US-09-944-457-82 (1-2284).

Qy 1 MetPheGlyGlyGluCysSerLeuThrValLeuValleCysPheLeuThr 20  
 Db 226 ATGTTCTTCGGGGAGAGAGGAGCTTGACTTACCTTTGGTAATAATTGCTTCTGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValleAsp 40  
 Db 286 CTAAGGCTGCTGCTAGTCAGAAATTCCTCAAAAAGAGTCTAGAAGATCTGTCATTGAC 345  
 Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
 Db 346 ATCCAGTCAATCTCTTCTTAAGGGAATCAGAGCAATGAGCCGCTATATATCTCAACTCA 405  
 Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGCATTAATTCCTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAC 465  
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGT 525  
 Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 Db 526 CCCAACGAGGAAGCCTGCTCATTTGAACCCAGCAAGAGGACTTATGAGTTACAGGATAAT 585  
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 Db 586 ACAGATTTTCCATCTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 645  
 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 Db 646 CTCTTACATGGCCAAATTTTCAACAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
 Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAGGCCACCGCATATCTCATGGAGAGACACACTTCTCAGAAGTTTGGATCCTCAGAT 765  
 Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200  
 Db 766 CACCTGGAGAACTATTTAAGATGATGAGCAAGTGCCTGCTTCTGTTATAAGAA 825  
 Qy 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
 Db 826 AAAGGCCATTTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGTTCATCTGCTGCT 885  
 Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 Db 886 GAAAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGT 945  
 Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTC 1005  
 Qy 261 GlnProGlnLeuAlaThrAlaProProValThrValThrValThrSerGlnProThr 280  
 Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTAAACCACTGTCTCCTCAGCCTCCACG 1065  
 Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
 Db 1066 ACCCTCATTTCTACAGTTTTTACACGGCTGCGGCTACACTCCAAGCAATGGCTCAACA 1125  
 Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACTACGGACTCGAAGGAGGAGCTTAGAACCATA 1185  
 Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
 Db 1186 CCGTTTACAGAAATCTCCAACTTAATTTGAACACAGGGAATGTGTATAAACCTACTGCA 1245  
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACCTGCTTCTCGGGAAGGTAG 1305  
 Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 Db 1306 GAGGCCAGTCAGGCAAGTTCTCCAGGGGAGTGTTCAGAAANAATCAGTACGCGCTTCCA 1365  
 Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValleGly 400

Db 1366 TTTGAAATGGCTTCTTATCGGTCCTGCTCTTTGGTGTCTTCTTGGTATAGGC 1425  
Qy 401 LeuValLeuLeuGlyArgLysSerGluSerLeuArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCCTCCCTGGGAGAGATCTTCGGAATCACTCCGCGAGAAACGTTACTCAAGACTG 1485  
Qy 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431  
Db 1486 GATATTGATCAATGGGATCTAATGTGCATC 1518

## RESULT 3

US-09-513-999C-9897  
; Sequence 9897, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 9897  
; LENGTH: 295  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 58  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 59  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 69  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 82  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 83  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 126  
; OTHER INFORMATION: k=g or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 129  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 133  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 136  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 158  
; OTHER INFORMATION: b=c or g or t  
US-09-513-999C-9897

## Alignment Scores:

Pred. No.: 6.49e-16 Length: 295  
Score: 242.00 Matches: 54  
Percent Similarity: 91.53% Conservative: 0  
Best Local Similarity: 91.53% Mismatches: 3  
Query Match: 10.95% Indels: 2  
DB: 4 Gaps: 0

US-10-735-014-83 (1-431) x US-09-513-999C-9897 (1-295)

Qy 375 AsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394  
Db 1 AATCAGTACGGCTTCCATTTGAAATAGCTTCTTATCGGTCCTGCTCTTTGGTATAGGC 60  
Qy 395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgLysSerGluSerLeuArg 414  
Db 61 CTGTTCTCTGTGATAGGCTTCRWCCCTCTGGGTAGATCTCTCGGAATCACTCCGAGG 120  
Qy 415 LysArg-TyrSerArg-LeuAspTyrLeuLeuAsnGlyIleTyrValAspIle 431  
Db 121 AAACGKTAMCTMAGRACTGGATTACTTGATCAATGGBATCTATGTGCATC 173

## RESULT 4

US-09-489-847-70  
; Sequence 70, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 1642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-489-847-70

## Alignment Scores:

Pred. No.: 1.07e-09 Length: 1642  
Score: 194.50 Matches: 105  
Percent Similarity: 37.06% Conservative: 64  
Best Local Similarity: 23.03% Mismatches: 166  
Query Match: 8.80% Indels: 121  
DB: 4 Gaps: 20

US-10-735-014-83 (1-431) x US-09-489-847-70 (1-1642)

Qy 20 ThrLeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValValle 39  
Db 289 AGCATCYCCTTAGCAGCAGCTCTGATCTCCCTGCGCAAGCAG---GAGGGAACCATTAGC 345  
Qy 40 AspileGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThr 59  
Db 346 AGCTGAGGAGCTGGCTGGCT---GGAGGCTCGGGACCGCCAGCCTGTCTCCAGCT 402  
Qy 60 GlnGluAspCysIleAsnSerCysThrLysAsn-----lleSerGlyAsp 76



Db 403 CACCCACAAGATGTGGACAGCTCTTGTGCTCATTTGGATTYYYTCCTTGCTTATCTCA 462  
QY 77 LysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyr 96  
Db 463 AAGCCATCGGGATCCAA-----CGATCCACG-----489  
QY 97 LeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu-----114  
Db 490 -----CAAATTGTCTCCATAACAAATGTGGGAAGGATTATGTCAA 528  
QY 115 -----Met 115  
Db 529 GAGGAATGCATCTGTGGAAACAGTTGATAATAAACGCTCTGAGGATGTAACCATGGCAGC 588  
QY 116 SerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeu 135  
Db 589 AGCTTCCTCTGTGCACATTGACCAAGAGGATTGGCAGCCCMCTCAACTCTATGGAAGTC 648  
QY 136 ProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHis 155  
Db 649 ACAACAGAGGACACA-----663  
QY 156 HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLys 175  
Db 664 ACAGGACAGATGTGATGAACCA-----GCAACTTCA 696  
QY 176 PheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeu 195  
Db 697 GGAGGTGCAGCTGATGTTGACCTCCATTGCTCCACGGCTGTGGCCTCCAGTAGCAGCT 756  
QY 196 LeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnLulile 215  
Db 757 GCGGCC-----TCCATTACGACTGCGCGCTCCAGTAGTACTGTG 795  
QY 216 AlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerPro 235  
Db 796 GCTCTCAGTGCTCCC---ACGACTGAGCCTCCAGTACAACTGTGGCCTCCATTGCTGCC 852  
QY 236 HisThr-----ThrSerAlaThrProLysProAlaThrLeu---LeuPro 249  
Db 853 ACGACTACAGCTCCAGTATGACTGGCGCTCCAGCACTCCCATGACACTTGCACCTCC 912  
QY 250 ThrAsnAlaSerVal-----ThrProSer-----GlyThrSerGlnProGln 263  
Db 913 GCGCCACAGCTCCACTTTCACAGGGGGACCCGCTCCATACCGCCACTGGGCATCATCT 972  
QY 264 LeuAlaThrThrAlaProValThrThrValThrSerGlnProProThrThrLeuile 283  
Db 973 CTCAGACAGCCCTCGCACAAGTCCCAAGAGAGCGCGTTCGCCAAGACACGACCCCTG 1032  
QY 284 SerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeu 303  
Db 1033 GCCAATGGCCACAGTGCT-----CAGACTGTAGCGACCCACACAAACACA 1080  
QY 304 ThrThrThrPheGlnAla---ProThrAspSerLysGlySerLeuGluThrIleProPhe 322  
Db 1081 AGCAGCCCCATGAGCACTCGTCCAAAGTCCCTCCAAAGCATGCCAGTGCACACCGCGCA 1140  
QY 323 ThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla-----340  
Db 1141 AGCCCTGTACCCCTCATGCT-----CCCCAAGCACAAAGT 1176  
QY 341 ---LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGly 359  
Db 1177 CCATTAGCAGGTGTACGTGACCGACCGCTGTGGTTAACACAA-----1221  
QY 360 ArgGluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeu 379  
Db 1222 -----NATAAATCCACAMCCATGCTCCCTCAACACACACACCCWAG 1260  
QY 380 ProPhe-----GluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394  
Db 1261 CCCCTCACCCAGCGCGTGTAGACAAACTCTCTCTGTGGTGTGCTGTACTCGGGGTG 1320

QY 395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArg 414  
Db 1321 ACCCTTTTCATCAGACTCTTGGTTTGTGGCTGCAGGCCTATGAGAGCTACAAGAAG 1380  
QY 415 LysArgTyrSerArgLeuAspTyrIleuIleAsnGlyIleTyrValAsp 430  
Db 1381 AAGGACTACACCCAGGTGGACTACTTAATCAACGGGATGTATGCCGAC 1428

## RESULT 5

US-09-774-528-230

; Sequence 230, Application US/09774528

; Patent No. 6743619

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Zhao, Qing A.

; APPLICANT: Yang, Yonghong

; APPLICANT: Xue, Aidong J.

; APPLICANT: Wehrman, Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Dunrui

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6743619el Nucleic Acids and

; FILE REFERENCE: Polypeptides

; CURRENT APPLICATION NUMBER: US/09/774,528

; CURRENT FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 441

; SOFTWARE: pf\_FL\_genes Version 2.0

; SEQ ID NO 230

; LENGTH: 1826

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (415)..(1764)

US-09-774-528-230

## Alignment Scores:

Pred. No.:	1,85e-09	Length:	1826
Score:	193.00	Matches:	126
Percent Similarity:	34.50%	Conservative:	61
Best Local Similarity:	23.25%	Mismatches:	170
Query Match:	8.73%	Indels:	187
DB:	4	Gaps:	23

US-10-735-014-83 (1-431) x US-09-774-528-230 (1-1826)

QY 20 ThrLeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValile 39  
Db 291 AGCATCCCTTAGCAGCAGCTCTGATCCCTTGGCCAAGCAG--GAGGGAACCATAGC 347  
QY 40 AsplleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThr 59  
Db 348 AGCCTGAGGAGCTGGCTGGCTGGGAGCCT-CGGGGACCGCCCGAGCTTGTCTCCAGCTCA 406  
QY 60 GlnGluAspCysValIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCys 79  
Db 407 CCCAAGATGGGACAGCTCTTGTGCTCA-----TTTGGATTTTCTCTCTGT 454  
QY 80 AsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePhe 99  
Db 455 CCTTATCTG-----AAAGCCATGGCGCATCCCAACAGCATCCACGCAAC-TTT 498  
QY 100 CysProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMet-----115  
Db 499 GTCCCTTAAC-----AAAAATGTGAAGGGATTAGTCAAGAGGAATGCA 540

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Qy 116 SerTyrArgIleIleThrAspPheProSer----- 125
|||
Db 541 TCTGTGAAACAGTTGATTAATAAAGCTCTGAGATGTAAACATGGCAGAGCTTCTCCT 600
|||
Qy 126 -----LeuThrArg-----
|||
Db 601 GTCACATTGACCAAGAGGACTTCGGCAGCCACCTCAACTCTATGGAAGTCACAACAGAG 660
|||
Qy 139 AspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThr 158
|||
Db 661 GACACA-----AGCAGGACA 675
|||
Qy 159 AspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySer 178
|||
Db 676 GATGTAGTGAACA-----GCAACTTCAGGAGTGTGCA 708
|||
Qy 179 SerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyr 198
|||
Db 709 GCTGATGTGTGACCTCCATTGCTCCACGGCTGTGGCTCCAGTACGACTGGCGCC--- 765
|||
Qy 199 LysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeu 218
|||
Db 766 -----TCCATTACGACTCGGCCTCCAGTATGACTGTGGCTCCAGT 807
|||
Qy 219 LeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThr--- 237
|||
Db 808 GCTCCC---ACGACTGAGCTCCAGTACACTGTGGCTCCATGTCTCCACACACTGCA 864
|||
Qy 238 -----ThrSerAlaThrProLysProAlaThrLeu-----LeuProThr 250
|||
Db 865 GCCTCCAGTATGACTGTGGCTCCAGCACTCCCATGACACTTGCACTCCCGGCCCAAG 924
|||
Qy 251 AsnAlaSerVal-----ThrProSer-----GlyThrSerGlnProGlnLeuAlaThr 266
|||
Db 925 TCCACTTCCACAGGCGGACCCGCTCCACTACGCCACTGGGCATCTCATCTCTCAGACA 984
|||
Qy 267 ThrAlaProProValThrThrValThrSerGlnProProThrThrLeuLeuSerThrVal 286
|||
Db 985 GCCCTGCACAAAGTGCCAAAGAGCAGCGGTGCCAAGACAGCAACCTGGCCACATTG 1044
|||
Qy 287 PheThrArgAlaAlaThrLeuGlnAlaMetAlaThrAla----- 301
|||
Db 1045 GCCACACGTGCT-----CAGACTGTAGCGACCCACAGCAAAACACAAGAGGCCCC 1092
|||
Qy 301 ----- 301
|||
Db 1093 ATGAGCACTCGTCCAAAGTCTTCCAAAGCACATGCCAGTGACACCGCGGCAAGCCCTGTA 1152
|||
Qy 301 ----- 301
|||
Db 1153 CCCCTATGCTGCCCAAGCACAAAGTCCCATTTAGCCAGGTGTCTAGTGGACCCCTGTG 1212
|||
Qy 302 ValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePro 321
|||
Db 1213 GTTAAACAACAATAATATCCACCCCATGCGCTCAAAACAACCCCGAGAGCCCGCCGCC 1272
|||
Qy 322 PheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeu 341
|||
Db 1273 ACCCCCAAGTG-----GTGACCACCAACCAAGGCACAAAGCCAGGAGCCCAACTGCCAGC 1326
|||
Qy 342 -----SerMetSer-----AsnVal 346
|||
Db 1327 CCAGTGCAGTACCTCACACAGGCCCAATCCCTGAGATGGAGGCCATGTCCCCACACACA 1386
|||
Qy 347 GluSerSerThrMetAsnLysThrAlaSerTrpGluGly----- 359
|||
Db 1387 CAGACAAGCCCATGCCATATACCCAGAGGAGCGTGGGCCGAGGCACATCCAGGCACCG 1446
|||
Qy 360 -----ArgGluAlaSerProGlySerSerSerGlnGlySerValProGluAsn 375
|||
Db 1447 GAGCAGGTAGAGACTGAAGCCACACACAGGTATGATTCTCCACTGTGGGCCAAACCCCGAGGC 1506
|||
```

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Qy 376 GlnTyrGly-----LeuPro----- 380
|||
Db 1507 TCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCAGCCAGCCAGCCAGCCAGTAC 1566
|||
Qy 381 -----PheGluLysTrpLeuLeuIleGly 388
|||
Db 1567 ATGCTGTGTACCACTGAGCCCTCACCCAGGCGGTGTAGACAAACACTCTCTTCTGGTG 1626
|||
Qy 389 SerLeuLeuPheGlyValLeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeu 408
|||
Db 1627 GTCTGTGTACTCGGGGTGACCCCTTTTCATCATCAGTCTTGTGTGGCTGCAGGCC 1686
|||
Qy 409 SerGluSerLeuArgLysArgTyrSerArgLeuAspTyrLeuIleAsnGlyIleTyr 428
|||
Db 1687 TATGAGAGCTACAGAAGAGGACTACACCCAGGTGGACTACTTATCAACGGGATGTAT 1746
|||
Qy 429 ValAsp 430
|||
Db 1747 GCGGAC 1752
|||

RESULT 6
US-09-799-451-412
; Sequence 412, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 412
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (325)..(1353)
US-09-799-451-412

Alignment Scores:
Pred. No.: 3,44e-06 Length: 1638
Score: 160.50 Matches: 66
Percent Similarity: 39.85% Conservative: 42
Best Local Similarity: 24.35% Mismatches: 114
Query Match: 7.26% Indels: 49
DB: 4 Gaps: 9

US-10-735-014-83 (1-431) x US-09-799-451-412 (1-1638)

Qy 147 SerGlnAlaValThrProLeuAlaHisHisThrAspTyrSerLysProThrAspIle 166
|||
Db 43 TCCCAACCAAGTCAACAGAGACTGTCTCCGGTGCCTGGAGCAAGGTGTTTGCAGTA 102
|||
```

```

QY 167 SerTrp-----ArgAspThrLeuSerGlnLysPheGly 177
Db 103 GACTTCCCATCCCTCGGACCCCAAGCGGGGACAGAAACCTCAACAACATCATCAGG 162
QY 178 SerSerAspHisLeu-----GluLysLeuPheLysMetAsp-----189
Db 163 AGTGGGAAAAATCTGCGCGCGACCTGAGGAGATCACCAGGCTCCAGTGGCGGAGCGAG 222
QY 190 -----GluAlaSerAlaGlnLeuLeuAlaTyr-----LysGluLys 201
Db 223 AGCCACCGGAGGTGAGCATTCGAACCTTGGCGGAGGTGTCAGTGCAGCGCTGAAGAG 282
QY 202 Gly-----HisSerGlnSerSerGlnPheSerSer-----AspGlnGlu 214
Db 283 GGCCTGGTGTGCGGACAGGACAGGAGGAGGACCTTCAAGATGTGCTCAACTACGAG 342
QY 215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValaLaser 234
Db 343 GTGGGTGTCTGTGCGGAGACCCCTAAAGGTGGCCCGTGACC-----TCCACA 393
QY 235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSer---253
Db 394 CTGTGTGACAGCTCTAGCACCCCTAGTGGGAGAGCCACCAGGCCAACTCCAGACACTCC 453
QY 254 -----ValThrProSerGlyThrSerGlnProGln 263
Db 454 TCTTGGCAGAAATCCAGGACAAACCACTTTGGTGACAAACCCAGCACAACTCCACTCCACAG 513
QY 264 LeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuIle 283
Db 514 ACCAGCACAACTCTGCTCTCAACCCAGCACAACTCTGCTCCACCAACCCAGCAAACT 573
QY 284 SerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeu 303
Db 574 TCTGCCCTACACACGACCAACCTCCACTCCAGACGACGATATCTCTGCCCTACAC 633
QY 304 ThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThr-----Ile 320
Db 634 AGCAGCACAACTCGGCTCTTCAAGCACACAACTCTGCTCGTACCAACGACGATAATC 693
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrAsnProThrAla 340
Db 694 TCTGCCCTTACACACGACCAACCTTTCTCCCTACCAACGACGACCAACCTCTGCTACTACA 753
QY 341 LeuSerMetSerAsnValGluSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db 754 ACCAGCACAACTCTGCCCTTACAGCACACAACTCCACTCCACGACGACGACGACAAACC 813
QY 361 GluAlaSerProGlySerSerGlnGlySer 371
Db 814 TCAGCTGCTTACAGCACAACTCCGCTTCT 846

RESULT 7
US-09-949-016-13892
; Sequence 13892, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13892
; LENGTH: 16562

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13892

Alignment Scores:
Pred. No.: 0.000474 Length: 16562
Score: 157.00 Matches: 106
Percent Similarity: 33.97% Conservative: 55
Best Local Similarity: 22.36% Mismatches: 176
Query Match: 7.10% Indels: 137
DB: 4 Gaps: 21

US-10-735-014-83 (1-431) x US-09-949-016-13892 (1-16562)
QY 22 ArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAspIle 41
Db 6133 AGGGCTCCCATCTCCCGAGCTGCTTAGCTCTAGCTCTCCATGATAGCTCCAACCTCT 6192
QY 42 Gln-----SerSerLeuSerLysGlyIleArgGlyAsnGluProVal 55
Db 6193 GAAAGGGACCCCTTCTCTCAGCTCCCTTAGCTCTGGTGGCTGGCTCCCA-----6246
QY 56 TyrThrSerThrGlnGluAspCysIleAsn-----Ser 66
Db 6247 ---CTCAGTTTCAAGAGGTTCTCTTTTCCACCTAACCTTCTTACTTCCCTCTTCACT 6303
QY 67 CysCysSerThrLysAsnIleSerGlyAspLysAla-----CysAsnLeuMetIle 83
Db 6304 GGCTGTAGCTCAGTCAGGTCAGTGATAACTCTGTGACCTCCCATTTGCTCTCAGAAC 6363
QY 84 PheAsp-----ThrArgLysThrAlaArgGln 92
Db 6364 AAAGACTAATCTTAATAAAGTTCCCTCTGAGTAGTCCCTAATCCAAAGGACCCCCAG 6423
QY 93 ProAsnCysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLys 112
Db 6424 CCCTCCATGTATAGTCAGTACTGT-----TCTTACCACCTGTGACCTCCCAT 6471
QY 113 GlyLeuMetSerTyrArgIleIleThrAspPheProSerLeu-----ThrArgAsnLeu 130
Db 6472 GGCCTC-----TATTCAATCTGGAGTGGCTCCCTTCTCAGACCAACCCCAACTAC 6525
QY 131 ProSerGlnGluLeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaVal 150
Db 6526 CCGTACCATCGTCTCCCTCCTCAAGTCAA-----6552
QY 151 ThrProLeuAlaHisHisHis-----ThrAspTyrSer---LysProThr-AspIle 166
Db 6553 -----AGATACCAACCATTTCTCAGTTCTGTATTTCTCCAAAAACCCAGGAAGCT 6603
QY 166 eserTrpArgAsp-----LysGluLys-----GlyHis 204
Db 6604 CAGCTGAAGGGGCTGTGTAGTCCACCTGTGCTTATCTCTTCACTCAGTCTCTTCC 6663
QY 171 -----ThrLeuSerGlnLys-----PheGly 177
Db 6664 TGTGTGACCTCTTCTCAAAAGACTGCGGGTCCCAACACCCCCAGATTTTCCCATTTTC 6723
QY 177 ySerSerAspHisLeuLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAla 197
Db 6724 TCTGGGCTCTCATCTTGACCTTTTACATCAGAGTTCTTTTGGTTCTCTCCTCAACTTTAGG 6783
QY 197 aTyr-----LysGluLys-----GlyHis 204
Db 6784 TCAACAGGCTCTAGTGTGTGTAGACCTTACAGAGAGACCATTTCTGTAGATCATTC 6843
QY 204 rGlnSer---SerGlnPheSerSerGlnGlnIleAlaHisLeuLeuProGluAsnVa 223
Db 6844 TTCCACAGGGGCTCTTATCTCTCAGAGATCTGTAAATCTCTCCCTCTCTCTCCAGAAA 6903
QY 223 lSerAlaLeuProAlaThrValAlaValaLaserProHisThrThrSerAlaThrProly 243
Db 6904 TGAGGTAGTTCTGTCTACTGTGGCTCTTCCAGTGGTGGCTCTTGTGACAAAGG 6963

```



```
/
/
/      1201 West Peachtree Street
/      CITY: Atlanta
/      STATE: Georgia
/      COUNTRY: USA
/      ZIP: 30309-3450
/
/      COMPUTER READABLE FORM:
/      MEDIUM TYPE: Floppy disk
/      COMPUTER: IBM PC compatible
/      OPERATING SYSTEM: PC-DOS/MS-DOS
/      SOFTWARE: Patent In Release #1.0, Version #1.25
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/09/241,581B
/      FILING DATE: 02-Feb-1999
/
/      CLASSIFICATION: <Unknown>
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Pabst, Patrea L.
/      REGISTRATION NUMBER: 31,284
/      REFERENCE/DOCKET NUMBER: MIT6620
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (404) 873-8794
/      TELEFAX: (404) 873-8795
/
/      INFORMATION FOR SEQ ID NO: 5:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 2032 base pairs
/      TYPE: nucleic acid
/      STRANDEDNESS: double
/      TOPOLOGY: linear
/      MOLECULE TYPE: cDNA
/      HYPOTHETICAL: NO
/      ANTI-SENSE: NO
/      FEATURE:
/      NAME/KEY: misc. feature
/      LOCATION: 40..1926
/      OTHER INFORMATION: /Function = "Nucleotides 40 through
/      1926 encode the amino acid sequence
/      for the Drosophila Melanogaster
/      Scavenger Receptor Class CI."
/      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
/
/      US-09-241-581B-5
/
/      Alignment Scores:
/      Pred. No.:          Length:          2032
/      Score:             148.00           Matches:          69
/      Percent Similarity: 36.0%           Conservative:       37
/      Best Local Similarity: 23.47%       Mismatches:       108
/      Query Match:       6.69%           Indels:           80
/      DB:                 3              Gaps:             9
/
/      US-10-735-014-83 (1-431) x US-09-241-581B-5 (1-2032)
/
/      QY 147 SerGlnAlaValThrProLeuAla-HisHisHisThrAspTyrSerLysProThrAsp11 166
/      Db 965 AGTGTGGCAACAAAGGATTAGCACCACACAGACCAACGCGCTCC-----GACAG 1015
/
/      QY 166 eSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLysLeuPh 186
/      Db 1016 GCAGCAACGACGACCAACCACTGGTCTACGATAT-----GATAAGTTGTT 1057
/
/      QY 186 eLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGluLysGlyHisSerGlnSe 206
/      Db 1058 CAGGTGCGATGCGGAACATCAATGTGGCGCTCCAAATATAACCAACAACTGATAGTCATGG 1117
/
/      QY 206 rSer-----GlnPheSerSerAsp----- 212
/      Db 1118 GATGTGGATGTAATGACGAGTGCCTTCGGATCAGACTTGTTCCTAACTATTGGAGG 1177
/
/      QY 213 -----GlnGluLeuAlaHis-LeuLeuProGluAsnValSerAlaLeuProAlaThrV 230
/      Db 1178 AGTCACAAAGGAGGTGCTCACCAGCAGGAGTATAGTATAGTCCCTGCCCAACG 1237
/
/      QY 230 alAlaValAlaSerProHisThr-----ThrS 239
/      Db 1238 TCACATCAACAAAGCAACAGCACTACGAGGAGTCAACAAACAAACCAACCAACGACGA 1297
```

```

239 erAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT 259
1298 CTACTACAGTACAAACAACAACTAAAGGCGCAACCAACCAACCAACCAACCAACGCGCA 1357
259 hrSerGlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProp 279
1358 CAACTACAAAGCGAACAACCAACCACTAAAGGCGCAACCAACCAACCAACCAACGCGCA 1417
279 ioThrThrLeuLeuSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlar 299
1418 CAACAACACGAGCTTCAACCAACCAAGTCTACAACTTCTTCAACGCTTCAACCTTCAA 1477
299 hrThrAlaValLeuThrThrPheGlnAlaProThrAspSerTyrGlySerLeuGluT 319
1478 CAACCAACGAGCAACCACTACAAATAAATGTGTTTACAAACAAGAAA----- 1524
319 hrLeuProPheThrGluLeuSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProT 339
1525 -----ACAAATAAATGATCCCTACTTCCAGTACCGAAGAAAGACTA 1564
339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrP- 357
1565 CAGGCATC-----ATCACCACTATGAACACGACGCGCAGCGCATCTTGGACG 1612
358 -----GluGlyArgGluAlaSerProGlySerSerGlnGlySerV 372
1613 TTGATCCTCAGGACATCGAGGTGCATGACACGAGCGGAAGTACCCCAATCCAGCTT 1672
372 alProGluAsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuLeuGlySerLeuLeuP 392
1673 TAGTA----- 1677
392 heGlyValLeuPheLeuValLeuGlyLeuValLeuLeu 404
1678 -----GTACTTACCTGCTACTCGGCATGTTCTGGTG 1710

RESULT 10
US-08-265-428-5
; Sequence 5, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2032 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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Db      1673  TAGTA-----1677
Qy      392  heGlyValleuPheLeuValIleGlyLeuValIleuLeu 404
Db      1678  -----GTACTTTTACTGCTACTCGGCATTTCTGGTG 1710

RESULT 11
PCT-US95-07721-5
; Sequence 5, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2032 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 40..1926
; OTHER INFORMATION: /Function = "Nucleotides 40 through
; OTHER INFORMATION: 1926 encode the amino acid sequence
; OTHER INFORMATION: for the Drosophila Melanogaster
; OTHER INFORMATION: Scavenger Receptor Class CI."
PCT-US95-07721-5

Alignment Scores:
Pred. No.: 9.8e-05 Length: 2032
Score: 148.00 Matches: 69
Percent Similarity: 36.05% Conservative: 37
Best Local Similarity: 23.47% Mismatches: 108
Query Match: 6.69% Indels: 80
DB: 5 Gaps: 9

US-10-735-014-83 (1-431) x PCT-US95-07721-5 (1-2032)
Qy      147  SerGlnAlaValThrProLeuAla-HisHisHisThrAspTySerIysProThrAspIle 166
Db      965  AGTGTGCGCAACGGATTATAGCACACACACAGACGAGTCC-----GACAG 1015
Qy      166  eSerTrpArgAspThrLeuSerGlnIysPheGlySerSerAspHisLeuGlnIysLeuPh 186
Db      1016  GCAGCAACACGACGACCACTGGTCTACGATAT-----GATAAGTTGTT 1057

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QY 186 elysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGlnSe 206
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1058 CAGGTCGATGCGGAACATCAATGTGCGCTTCAATATAACCAACAATGATAGTATGATGG 1117
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 206 rSer-----GlnPheSerSerAsp----- 212
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1118 GATGGGATGTAATGACGAGTGCCTTTCGGATGAGACTGTGTCCTAAACTATTGGAGG 1177
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 213 -----GlnGluAlaHis-LeuLeuProGluAsnValSerAlaLeuProAlaThrV 230
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1178 AGTGCAAAAGGAGCTGCTCACACGACGAGGATGATATTAGTTCCTGCCCAACGG 1237
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 230 alalavalalaserProHisThr-----ThrS 239
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1238 TCACATCAACAAGCAAGCACTACGAGGAAGTCAACAACAACAACAACAAGCACGA 1297
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 239 eAlaAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT 259
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1298 CTAACAAGTCAACAACAACCTAAAGGCCCAACCAACCAACAACAACAAGGCCA 1357
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 259 hrSerGlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProP 279
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1358 CAACTACAAAGCGAACAACAACCTAAACCAACCAACCAACCTTCAACAACGCCGACG 1417
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 279 roThrThrLeuLeuSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaT 299
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1418 CAACAACAACGACTTCAACAACAACAACCTTCAACAACCTTCAACAACCTTCAA 1477
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 299 hrThrAlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluT 319
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1478 CAACACCAACGACAACAACCTAATAATGTGTTTACACAACAAGAAA----- 1524
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 319 hrIleProPheThrGluIleSerAsnLeuLeuLeuAsnThrGlyAsnValTyrAsnProT 339
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1525 -----ACACAATAATGATCCCTACTTCCAGTACCGAAAAGACTA 1564
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrp---- 357
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1565 CAGGCATC-----ATCACCAACATGAAGACACGCAAGCGCATCTTGGAAAG 1612
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 358 -----GluGlyArgGluAlaSerProGlySerSerSerGlnGlySerV 372
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1613 TTGATCCTCAGACATCGAGGTCAATGACACGAGCGGAAGTACCCCAATCCAGCTT 1672
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 372 alProGluAsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuIleGlySerLeuLeuP 392
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1673 TAGTA----- 1677
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 392 heGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1678 -----GTACTTTACCTGCTACTCGCGATTGTTCTGTG 1710
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

## RESULT 12

```

US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12147

```

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; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

```

## Alignment Scores:

```

Pred. No.: 5.74 Length: 767677
Score: 146.00 Matches: 81
Percent Similarity: 37.36% Conservative: 21
Best Local Similarity: 29.67% Mismatches: 120
Query Match: 6.60% Indels: 51
DB: 4 Gaps: 14
US-10-735-014-83 (1-431) x US-09-949-016-12147 (1-767677)
QY 88 LysThrAlaArgGlnProAsnCysTyr---LeuPhePheCysProAsnGluGluAlaCys 106
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753296 AAGGAAGCGCGTGGCCACCATGTACCCACACAGACACTGTGCAGCCACAGCCAGCATGC 753237
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 107 ---ProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIleThrAspPheProSer 125
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753236 ACCCCACACACCCCA-----CTATCACACACCCCAACACACCCACAGCCACCA 753189
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 126 LeuThrArgAsnLeuPro-SerGlnGluLeuProGlnGluAspSerLeuLeuHisGlyG1 145
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753198 CACACCCACAGCACCCCGACGCCATCACACCCCAACAGCCACCAACCCACAGCCA 753129
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 145 nPheSerGln-----AlaValThrProLeuAlaHis----- 155
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753128 CCAGCATCCACAGCCACCCAGCCACCCACACACCCCAACCCATCACACACCCACGG 753069
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 156 HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnly 175
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753068 GCACACACACCCCAACAGCCACCCACACACCCCAACCCCAACCCCAACCCCAACCA 753009
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 175 sPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLe 195
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 753008 CACAACCCACAGCCACCAACACAC----- 752984
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 195 uLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnIu1 215
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752983 -----CACAGCCATCCACCCACAGCCACCCACAGCCACCCACCA 752946
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 215 eAlaHisLeuLeuProGluAsnValSerAlaLeu-ProAlaThrVal---AlaValAlaS 234
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752945 CAGCCACACAGCACCCCAACAGCCACCGCATCCACAGCCACCAACACACCCCAACCA 752886
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 234 erProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerV 254
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752885 GCACGACCCCATGGGACCCAGCCACCCCAACAGCCACCAACCCCAACCAACCA 752829
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 254 alThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr---- 272
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752828 TGACCCCATGGGACCAACAGCCACCC-----ACAGCCACCAACCAACCCCAACCA 752772
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 273 -----ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaA 291
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752771 ACCCCACAGCCACCAACAACCCAGCCACCCCAACAGCCACCAACCAACCA 752712
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 291 laAlaThrLeuGlnAlaMetAlaThrAlaThrAlaValLeuThrThrPheGlnAlaProT 311
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752711 CAGCTGGGACACACCCCATGACCCACCACTCCACAGCCACCAACCAATAC----- 752658
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 311 hrAspSerLysGlySerLeuGluThrIle-ProPheThrGluIleSerAsnLeuThrLeu 330
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 752657 CA-----GGAGCCATGCACCTCTATGGCCACTGCACACCCCTGTGCTACTGACCACA 752607
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 331 Asn---ThrGlyAsnValTyrAsnProThrAla 340
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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QY 278 ProProThrThrLeuLeuSerThrValPheThrArgAlaAlaThrLeuGlnAlaMet 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1810 CCAGAGACTGCCACACCTCCACAGTGTATCCACCGCCACCAACAGGGGCCACC 1751

QY 298 Ala-----ThrAlaValLeuThr 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1750 GGCTGTGTGGCCACCCCTCTCCACCCAGGAACAGCTCACACTACCAAGTGGCGACT 1691

QY 305 ThrThrPheGln-----AlaProThrAspSerLysGlySerLeuGluThrIle 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1690 ACCACAAACCGGGCTTCACAGTCACCCCTCTCTCAGCCAGGAGCGCAGCGCCT 1631

QY 321 ProPheThrGluLeuSerAsnLeuThrLeuAenThr----- 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1630 CCA---GTGTGGATCAGCAACACCAACCAACAGGTGGCTTCCAGGTGACCCCC 1574

QY 333 -----GlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSer 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1573 TCCTCGTCCCGGGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1514

QY 349 SerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSer 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1513 GCCACT-----GGTCTATGCAACACCCCTCTCTAGCACA 1478

QY 369 GlnGlySer-ValProGluAsnGlnTyrGlyLeuProPheGluLys 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1477 CAGACCAAGTGGTACCTCGTGGCGAATTCGGCACCGGGCTGACAAG 1432
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## RESULT 15

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US-09-854-133-158/c
; Sequence 158, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-158
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Alignment Scores:
Pred. No.: 0.00019 Length: 2114
Score: 145.50 Matches: 63
Percent Similarity: 40.74% Conservative: 25
Best Local Similarity: 29.17% Mismatches: 66
Query Match: 6.58% Indels: 62
DB: 4 Gaps: 9
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US-10-735-014-83 (1-431) x US-09-854-133-158 (1-2114)

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QY 204 SerGlnSerSerGlnPheSerSerGlnGlnLeuAlaHisLeuLeuProGluAsnVal 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1999 TCCAAAGCCACTCCCTCTCTCAGT-----CCAGGGACTGCA 1964

QY 224 SerAlaLeuProAlaThrValAlaValAla-----SerProHisThrSerAlaThrPro 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1963 ACCGCCCTTCCAGCTGAGAGAGACAGCCACCAACCAACCAACCAACCAACCAACCA 1904

QY 243 LysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnPro 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1903 ATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1871
```

```
QY 263 GlnLeuAlaThrThrAlaProProValThrThrVal-----ThrSerGln 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1870 CGCCTATCAGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1811

QY 278 ProProThrThrLeuLeuSerThrValPheThrArgAlaAlaThrLeuGlnAlaMet 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1810 CCAGAGACTGCCACACCTCCACAGTGTATCCACCGCCACCAACAGGGGCCACC 1751

QY 298 Ala-----ThrAlaValLeuThr 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1750 GGCTGTGTGGCCACCCCTCTCTCCACCCAGGAACAGCTCACACTACCAAGTGGCGACT 1691

QY 305 ThrThrPheGln-----AlaProThrAspSerLysGlySerLeuGluThrIle 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1690 ACCACAAACCGGGCTTCACAGTCACCCCTCTCTCAGCCAGGAGCGCAGCGCCT 1631

QY 321 ProPheThrGluLeuSerAsnLeuThrLeuAenThr----- 332
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1630 CCA---GTGTGGATCAGCAACACCAACCAACCAACCAACCAACCAACCAACCA 1574

QY 333 -----GlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSer 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1573 TCCTCGTCCCGGGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1514

QY 349 SerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSer 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1513 GCCACT-----GGTCTATGCAACACCCCTCTCTAGCACA 1478

QY 369 GlnGlySer-ValProGluAsnGlnTyrGlyLeuProPheGluLys 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1477 CAGACCAAGTGGTACCTCGTGGCGAATTCGGCACCGGGCTGACAAG 1432
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Search completed: April 27, 2005, 01:07:23  
Job time : 575 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: April 26, 2005, 23:55:07 ; Search time 644 Seconds  
(without alignments)  
4063.079 Million cell updates/sec

Title: US-10-735-014-83

Perfect score: 2211

Sequence: 1 MFPGEGSLTYTLVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO\_spool\_p/US10735014/runat\_26042005\_113103\_7512/app\_query.fasta\_1.503  
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-LOOPCL=0 -LOOPEXT=0 -UNITIS=bits -START=1 -END=-1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USRP=US10735014 @CGN 1.1 723 @runat\_26042005\_113103\_7512  
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications\_NA:  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
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21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	2284	9	US-09-866-028-82
2	2211	100.0	2284	9	US-09-989-722-514
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8	2211	100.0	2284	9	US-09-944-457-82
9	2211	100.0	2284	9	US-09-989-732-514
10	2211	100.0	2284	9	US-09-991-073-514
11	2211	100.0	2284	9	US-09-945-587-82
12	2211	100.0	2284	9	US-09-990-442-514
13	2211	100.0	2284	9	US-09-991-163-514
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21	2211	100.0	2284	9	US-09-989-721-514
22	2211	100.0	2284	9	US-09-943-851A-82
23	2211	100.0	2284	9	US-09-944-413-82
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# ALIGNMENTS

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; Sequence 82, Application US/09866028  
; Patent No. US20020058309A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel



1	PRIOR FILING DATE: 1998-06-12	
2	PRIOR APPLICATION NUMBER: 60/089440	
3	PRIOR FILING DATE: 1998-06-16	
4	PRIOR APPLICATION NUMBER: 60/089512	
5	PRIOR FILING DATE: 1998-06-16	
6	PRIOR APPLICATION NUMBER: 60/089514	
7	PRIOR FILING DATE: 1998-06-16	
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1 PRIOR APPLICATION NUMBER: 60/090862  
2 PRIOR FILING DATE: 1998-06-26  
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4 PRIOR FILING DATE: 1998-06-26  
5 PRIOR APPLICATION NUMBER: 60/091360  
6 PRIOR FILING DATE: 1998-07-01  
7 PRIOR APPLICATION NUMBER: 60/091478  
8 PRIOR FILING DATE: 1998-07-02  
9 PRIOR APPLICATION NUMBER: 60/091544  
10 PRIOR FILING DATE: 1998-07-01  
11 PRIOR APPLICATION NUMBER: 60/091519  
12 PRIOR FILING DATE: 1998-07-02  
13 PRIOR APPLICATION NUMBER: 60/091626  
14 PRIOR FILING DATE: 1998-07-02  
15 PRIOR APPLICATION NUMBER: 60/091633  
16 PRIOR FILING DATE: 1998-07-02  
17 PRIOR APPLICATION NUMBER: 60/091978  
18 PRIOR FILING DATE: 1998-07-07  
19 PRIOR APPLICATION NUMBER: 60/091982  
20 PRIOR FILING DATE: 1998-07-07  
21 PRIOR APPLICATION NUMBER: 60/092182  
22 PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 1,47e-211 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x US-09-989-722-514 (1-2284)

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QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValValIleAsp 40  
DB 286 CTAGGCTGTCTGCTAGTACAGANTTGCTCAAAAGAGCTAGAGAGTGTGTCAATTGAC 345  
QY 41 IleGlnSerSerLeuSerLysGlyLeuArgGlyAsnGluProValThrThrSerThrGln 60  
DB 346 ATCCAGTCTATCTTCTTAAGGAATCAGAGCAATGAGCCGCTATATCTCAACTCAA 405  
QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
DB 406 GAAGACTGCATTAATCTTCTTAAGGAATCAGAGCAATGAGCCGCTATATCTCAACTCAA 465  
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
DB 466 TTGATGATCTTCGACACTCGAANAACAGCTAGACACCCAACTGCTACTATTTTCTGT 525  
QY 101 ProAsnGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgIleIle 120  
DB 526 CCCAACGAGGAAGCTGTCCATTGAACCCAGAAAAGGACTATGAGTTACAGGATAATT 585  
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnLysSer 140  
DB 586 ACAGATTTCCTCTTCAACAGAAAATTTGCAAGCCAGAGATTACCCAGGAAGATTCT 645  
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
DB 646 CTCTTACATGCCCAATTTTCACAGCAGCTACTCCCTAGCCCATCATCACAGATTAT 705  
QY 161 SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
DB 706 TCAAGGCCCAACCGATATCTCATGAGACACACTTTCTCAGAAGTTGGATCTCAGAT 765  
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200  
DB 766 CACCTGGAGAAATATTATTAAGATGATGAAGCAAGTGCACAGCTCTTGTCTTAAAGAA 825

QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
DB 826 AAAGGCCATTTCTCAGAGTTTCTCCTGATCAAGAAATAGCTCATCTGCTGCT 885  
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
DB 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGCT 945  
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
DB 946 ACTCCAAAGCCGCCACCTTACCCCACTTCTCAGTGACACCTTCTGGGACTTCC 1005  
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
DB 1006 CAGCCACAGTGGCCACACAGCTCCACCTGTAACTGTCACTTCTGAGCTCCACG 1065  
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DB 1186 CCGTTTACAGAAATCTCCAACCTTAACTTTGAAACACAGGGAATGTGTATAACCTTACGCA 1245  
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DB 1246 CTTTCTATGTCAAAATGTGAGTCTTCCACTATGAATAAAACTGCTTCTCGGAAGGTAGG 1305  
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
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QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
DB 1366 TTTGAAAATGGCTTCTTATCGGCTCCCTGCTCTTTGGTGTCTGTTCTTGGTGATAGGC 1425  
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420  
DB 1426 CTGCTCTCTCTGGGTAGAATCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485  
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
DB 1486 GATTAATTGATCAATGGATCTATGTGGACATC 1518

## RESULT 3

US-09-989-723-514  
; Sequence 514, Application US/09989723  
; Patent No. US20020072092A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Pao, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 1,47e-211 Length: 2284  
 Score: 2211.00 Matches: 431  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x US-09-989-723-514 (1-2284)

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 Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40  
 Db 286 CTAAGGCTGTCTGCTAGTACAGAAATTCCTCAAAAAGAGCTAGAGAAGATGTTGTCAATTGAC 345  
 Qy 41 IleGlnSerLeuSerLeuGlyGlyLeuArgGlyAsnGluProValTyrThrSerThrGln 60  
 Db 346 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGGCAATGAGCCGTAATATCTTCAACTCAA 405  
 Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 Db 406 GAAGACTGCATTAATTCCTGCTTCAACAAAAACATATCAGGGGCAAAAGATGTAAC 465  
 Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 Db 466 TTGATGATCTTCGACACTCGAAAAACACAGCTAGACAAACCCAACTGCTATTTTCTGT 525  
 Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 Db 526 CCCACGAGGAGGCTGCTCCATTGNAACCAACAAAGGACTTATGAGTTACAGGATTAAT 585  
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnLysAspSer 140  
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 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 Db 646 CTCATTACATGCCAAATTTTCAAGAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705

Qy 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAGCCCAACCGATATCTCATGGAGAGACACACTTCTCAGAAAGTTTGATCTCTAGAT 765  
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 Db 766 CACCTGGAGAAACTATTATTAAGATGGATGAAGCAAGTCCCGAGCTCTCTGTCTATAAGAA 825  
 Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlnIleAlaHisLeuLeuPro 220  
 Db 826 AAAGGCCATTTCTCAGAGTTCCACAATTTCTCTGATCAAGAAATAGTCTATCTGCTCCT 885  
 Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 Db 886 GAAATGTGAGTGGCTCCCGAGCTACGGTGGAGTGTCTTCTCCACATACACCTCGGCT 945  
 Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCCAAAGCCCGCCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
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 Db 1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245  
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
 Db 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATGATATAAACTGCTTCTGGGAAGTAGG 1305  
 Qy 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
 Db 1306 GAGGCCAGTCCAGGAGTCTCTCCAGGCGAGTGTCCAGAAATCAGTACGGCTTCCA 1365  
 Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuPheGlyValLeuPheLeuValIleGly 400  
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCCTGGTGATAGGC 1425  
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
 Db 1426 CTGTCTCTCTGGGTAGATCTTTCGATATCACTCCGAGGAAACGTTACTCAAGACTG 1485  
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## RESULT 4

US-09-989-279-514  
 ; Sequence 514, Application US/09989279  
 ; Patent No. US20020072496A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.



APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
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Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAapValIleasp 40
Db 286 CTAAGGCTGTCTGCTAGTCAGAAATGCTCAAAAGAGCTAGAGAGTGTGTGATTGAC 345

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
Db 346 ATCCAGTCACTCTTTCTTAAGGGAATCAGAGCAATGAGCCGTATATACCTCACTCAA 405

Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 406 GAAGACTGCATTAATCTTGTCTGTTCACAAAAACAATATCAGGGGACAAAGCATGAAC 465

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACTATTTTCTGT 525

Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120

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Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCCAGAGTTATCCCCAGGAAGATTCT 645
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
Db 646 CTCTTATAGGCAATTTTCAAGCAGTCACTCCCTAGCCATCATCACAGATTAT 705
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Db 706 TCAAGGCCACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAAACTATTATTAAGATGGATGAAGCAAGTCCCGAGCTCCTTGTGTTAAGGAA 825
Qy 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db 886 GAAATGCTGAGTGGCTCCCGAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCT 945
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 946 ACTCCAAAGCCCGCACCTTTACCCACCAATGCTTCACTGACACACCTTCTGGGACTTCC 1005
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1306 GAGGCCAGTCCAGGCAATCTCCCGAGGAGGAGTTCAGAGAAATCAGTACGGCTTCCA 1365
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Db 1366 TTTGAAAANAAGGCTTCTTATTCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGGGTATAGG 1425
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Db 1426 CTGCTCTCTCTGGGTAGAATCTTTTCGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485
Qy 421 AspTyrIleLeuLeuGlyArgIleTyrValAspIle 431
Db 1486 GATTATTGTCAATGGGATCTATGTGGACATC 1518

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## RESULT 5

US-09-989-727-514  
; Sequence 514, Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Klijavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730PIC65  
 ; CURRENT APPLICATION NUMBER: US/09/989,727  
 ; CURRENT FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
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 ; PRIOR FILING DATE: 1998-02-25  
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Db 1486 GATTATTGATCATGGGATCTATGTGGACATC 1518

RESULT 6

US-09-944-449-82

Sequence 82, Application US/09944449

Patent No. US20020102647A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Ferraro, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kljavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548PIC1

CURRENT APPLICATION NUMBER: US/09/944,449

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR FILING DATE: December 15, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR FILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,702

PRIOR FILING DATE: December 15, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR FILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/068,017

PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/070,440

PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/074,092

PRIOR FILING DATE: February 9, 1998

PRIOR APPLICATION NUMBER: 60/075,945

PRIOR FILING DATE: February 25, 1998

PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 60/113,296

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999

PRIOR APPLICATION NUMBER: PCT/US98/19330

PRIOR FILING DATE: September 16, 1998

PRIOR APPLICATION NUMBER: PCT/US98/25108

PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021

PRIOR FILING DATE: December 16, 1998

PRIOR APPLICATION NUMBER: 09/218,517

PRIOR FILING DATE: December 22, 1998

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR FILING DATE: March 3, 1999

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: June 22, 1999

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409

PRIOR FILING DATE: No. US20020102647A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: No. US20020102647A1ember 30, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28301

PRIOR FILING DATE: December 1, 1999

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: February 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: March 2, 2000

PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: May 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: July 28, 2000

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: December 1, 2000

PRIOR APPLICATION NUMBER: PCT/US01/06520

PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 82

LENGTH: 2284

TYPE: DNA

ORGANISM: Homo Sapien

US-09-944-449-82

Alignment Scores:

Pred. No.:	1.47e-211	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x US-09-944-449-82 (1-2284)

QY 1 MetPheGlyGlyGlySerLeuThrTyrThrLeuValIleCysPheLeuThr 20

Db 226 ATGTTCTTCGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACA 285

QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleApp 40

Db 286 CTAAGGCTGTCTGTAGTACAGAAATTCCTCAAAAAGAGCTTAGAGATGTTCTTCTTAC 345

QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db 346 ATCCAGTCATCTCTTTCAGGGAATCAGAGCAATGAGCCGTAATATATATCTCACTCAA 405

QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80

Db 406 GAAGACTGCATTAAATTCCTGCTTTCAACAAAAACATATCAGGGGACCAAGCATGTAAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCACTGCTACTATTTTCTGT 525

QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120

Db 526 CCCAACGAGGAGCCTGTCCATTGAACACAGAAAAGGAGCTTATGAGTTACAGGTAAT 585

QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

Db ACAGATTTCCTCTTCCAGCAAAATTTGCCAGGCAAGATTACCCAGGAAGATTCT 645  
QY LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db CTCTTACATGGCAATTTTCAAGAGCAGTCACTCCCTTAGCCCATCATCACAGATTAT 705  
QY SerLysProThrAspLysThrArgAspThrLysSerGlnLysPheGlySerSerAsp 180  
Db TCAAGGCCCCCGGATATCTCATGGAGACACACTTCTCAGAAGTTGGATCTCTCAGAT 765  
QY HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db CACCTGGAGAACTATTTAAGATGATGATGATGATGATGATGATGATGATGATGAT 825  
QY LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220  
Db AAAGGCCATCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAATAGTCTCTCTGCT 885  
QY GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db GAAATGTGAGTGGCTCCAGCTTACGGTGGCAGTTGCTTCTCCACATACCACTCGCT 945  
QY ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
QY GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db CAGCCACAGCTGGCCACACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCTCCACG 1065  
QY ThrLeuLysThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db ACCCTCATTTCTACAGTTTTCACGGCTCGGCTACCTCCAAAGCAATGGCTACAA 1125  
QY AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db CGAGTTCTGACTACCACTTTCAGGCACCTACGAGCTCGAAAGGAGCTTAGAAACCAT 1185  
QY ProPheThrGluLysSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db CCGTTTACAGAAATCTCCAACTTAATTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245  
QY LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db CTTTCTATGTCAAATGTGGAGTCTTCCACTATGATATAAACTGCTTCTCGGAAAGTAGG 1305  
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Db GAGCCAGTCAGGAGTCTCTCCAGGCGAGTGTTCAGAAATCAGTACGGGCTTCCA 1365  
QY PheGluLysTrpLeuLeuLysGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
Db TTTGAAANAAGCTTCTTATCGGTCCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1425  
QY LeuValLeuLeuGlyArgGlyLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
Db CTGCTCTCTCTGGGTAGATCTTTCGGATCATCTCCGAGAAACGTTACTCAAGACTG 1485  
QY AspTyrLeuLysLeuGlyValLeuValAspIle 431  
Db GATTATTGTGATCAATGGGATCTATGTGACATC 1518

## RESULT 7

US-09-989-731-514  
; Sequence 514, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone  
APPLICANT: Rong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730F1C70  
CURRENT APPLICATION NUMBER: US/09/989, 731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
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; PRIOR APPLICATION NUMBER: 60/088217  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR APPLICATION NUMBER: 60/090444  
; PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/090445  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090676  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090678  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090690  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090694  
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; PRIOR APPLICATION NUMBER: 60/090695  
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; PRIOR APPLICATION NUMBER: 60/090696  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090862  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.:	1,47e-211	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x US-09-989-731-514 (1-2284)

Qy	1	MetPhePheGlyGlyGluGlySerLeuThrTyThrLeuValIleCysPheLeuThr	20
Db	226	ATGTTCTTTCCGGGGAGAGGGAGCTTGACTTTGGTAATAATTTGCTTCTGTGACA	285
Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleLeu	40
Db	286	CTAAGGCTGTCTGTAGTCAGAAATTCCTCAAAAGAGCTTAGAAGATGTTGTCATTGAC	345
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGAATCAGAGCAATGAGCCGTATATACTTCAACTCAA	405
Qy	61	GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	406	GAAGACTGCATTAATTTCTTGTCTTCAACAAAAAACAATATCAGGGGCAAAAGCATGTAAAC	465



Qy	81	LeuMetIlePheAspThrArgLysThrAlaIaArgGlnProAsnCysTyrLeuPhePheCys	100
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACACACCACTCTTACCTATTTTCTGT	525
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120
Db	526	CCCACGAGGAGGAGCTGTCCATTGAAACACGACAAAGGACTTATGAGTTACAGGATAATT	585
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
Db	586	ACAGATTTTCCATCTTTGACACAGAAATTTGCCAAAGCCACAGAGTTTACCCAGGAAGATTCT	645
Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisIleThrAspTyr	160
Db	646	CTCTTTACATGGCCAAATTTTCAACAGCAGTCACTCCCTAGCCCCATCATCACACAGATTAT	705
Qy	161	SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp	180
Db	706	TCAAAGCCCACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCTCTCAGAT	765
Qy	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200
Db	766	CACCTGGAGAAACTATTTAAGATGCATCAAGCAAGTGCCAGCTCCTTGCTTTATAAGGAA	825
Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnLutIleAlaHisLeuLeuPro	220
Db	826	AAAGCCATTTCTCAGATTACAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTCT	885
Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
Db	886	GAATAATGTAGTGGCTCCAGCTACCGTGGCAGTTGCTTCTCCACATACCACTCGGCT	945
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	946	ACTCCAAGCCCGCCACCCCTTCTACCCACCAATGCTTCAGTGCACCTTCTGGGACTTCC	1005
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
Db	1006	CAGCCACAGCTGGCCACCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCCACG	1065
Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1066	ACCCCTCAATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTTACAACA	1125
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1126	GCAGTTCTGACTACCACTTTCAGCCACCTACGGACTCGAAAGCAGCACTTAGAAACCATTA	1185
Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1186	CCGTTTACAGAAATCTCCAATTAACCTTGAACACAGGGAATGTGTATACCCCTACTGCA	1245
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1246	CTTTCTATGTCAAATGTGGAGTCTTCACATATGAATATAAACTGCTTCTCTGGGAAGGTAGG	1305
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1306	GAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAATCAGTACGGCTTCCA	1365
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAATAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCCTGGTATAGGC	1425
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu	420
Db	1426	CTCGTCTCTCGGTAGAAATCTTTCCGAATCACTCCGACGGAACGTTTACTCAAGACTG	1485
Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1486	GATTATTGTGATCAATGGGATCTATGTGGACATC	1518

US-09-944-457-82  
; Sequence 82, Application US/09944457  
; Patent No. US20020110859A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
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; PRIOR FILING DATE: December 17, 1997  
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; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999



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; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-457-82

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Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x US-09-944-457-82 (1-2284)

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Db 286 CTAAGGCTGCTGCTAGTACAGAAATGGCTCAAAAAGAGTCTAGAAGATGTTGCTATTGAC 345

QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrGln 60
Db 346 ATCCAGTGCATCTCTTCTAAGGGAATCAGAGGCAATGAGCCGATATATCTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 406 GAAGACTGATTAATTTCTGTTCAACAAAACATATCAGGGGACAAACATGTATAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysPheLeuPheCys 100
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACCAACCACTGCTACCTATTTTCTGT 525

QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgIle 120
Db 526 CCCAACGAGAGACCTGCTCCATTGAACACGAGAAAAGGACTTATGAGTTACAGGATAAT 585

QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCAAGAGTATACCCAGGAAGATTCT 645

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QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 706 TCANAAGCCCAACCGATATCTCATGGAGACACACTTTCTCAGAAGTTTGGATCTCAGAT 765

QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAAACTATTTAAGATGATGAAGCAAGTCCAGCTCCTCTCTTATAGGAA 825

QY 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
Db 826 AAAGGCCATTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAATAGCTCATCTGTGCT 885

QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
Db 886 GAAATGTGAGTGGCTCCAGCTAGGTGGAGGTGCTTCTTCCACATACCACTCGGCT 945

QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 946 ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCACTGACACCTTCTGGGACTTC 1005

QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280
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QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTTGGTGTCTCTGCTGTGATAGGC 1425

QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgGlyArgTyrSerArgLeu 420
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QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

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APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
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CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-735-014-83 (1-431) x US-09-989-732-514 (1-2284)

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DB 286 CTAAGGCTGCTGCTAGTACAGAAATGCTTCAAAAAGAGTCTAGAAGATGTTGCTATTGAC 345

QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
DB 346 ATCCAGTCAATCTTTTCTAAGGGAATCAGAGGCAATGAGCCGCTATATCTTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 406 GAAGACTGCTAATTAATTTCTGCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPheCys 100
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## RESULT 10

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US-09-991-073-514
; Sequence 514, Application US/09991073
; Patent No. US20020127576A1

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QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
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QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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DB 1486 GATTATTGATCAATGGGATCTATGTGACATC 1518

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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deonoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC15  
CURRENT APPLICATION NUMBER: US/09/991.073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,476-211 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-735-014-83 (1-431) x US-09-991-073-514 (1-2284)

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Db 226 ATGTTCTTGGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40
Db 286 CTAAAGGCTGCTGCTAGTCAGAAATTCCTCAAAAGAGCTAGAGAGTTGTCTATTCAC 345

Qy 41 IleGlnSerLeuSerLysGlyIleArgGlyAsnGluProValThrSerThrGln 60

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Db 346 ATCCAGTCATCTCTTTCTTAAGGGAATCAGAGGCAATGAGCCCGTATATATCTCAACTCAA 405
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Db 406 GAAGACTGCATTAAATCTTGTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAAC 465
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrIleuPhePheCys 100
Db 466 TTGATGATCTTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGT 525
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
Db 526 CCCAACGAGGAAGCCTGTCCATTGAACCCAGCAAAAGGACTTATGAGTTACAGGATAAT 585
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
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Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 706 TCAAAAGCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAACTATTTAAGATGATGAAGCAAGTGGCCAGCTCTTGTCTTATAAGAA 825
Qy 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220
Db 826 AAAGGCCATTTCTCAGAGTTCAAAATTTTCTGTATCAAGAAATAGCTCATCTGTCCT 885
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProThr 280
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTGTAACTGTCTCAGTGACACCTTCTGGGACTTCC 1065
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
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Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1306 GAGGCCAGTCAGGAGATTTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCTTCCA 1365
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTTCTCTGGTGATAGC 1425
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGlnSerLeuArgLysArgTyrSerArgLeu 420
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## RESULT 11

US-09-945-587-82  
; Sequence 82, Application US/09945587  
; Patent No. US20020127643A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,587  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
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; PRIOR APPLICATION NUMBER: 60/069,278  
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; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
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; PRIOR FILING DATE: December 17, 1997  
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; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
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; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021  
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; PRIOR APPLICATION NUMBER: 09/218,517  
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; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
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; PRIOR FILING DATE: February 28, 2001  
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; SEQ ID NO 82  
; LENGTH: 2284  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-945-587-82

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Query Match: 100.00% Indels: 0  
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US-10-735-014-83 (1-431) x US-09-945-587-82 (1-2284)

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QY 161 SerLysProThrAspPheSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
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QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
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QY 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220  
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QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
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Db 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCACTGACACCTTCTGGGACTTCC 1005  
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
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QY 421 AspTyrLeuLeuAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTTGATCAATGGGAATCTATGTGGACATC 1518

## RESULT 12

US-09-990-442-514  
; Sequence 514, Application US/09990442  
; Patent No. US20030132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC8  
; CURRENT APPLICATION NUMBER: US/09/990,442  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1,47e-211	Length:	2284
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-735-014-83 (1-431) x US-09-990-442-514 (1-2284)

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Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuIleGlySerLeuGluAspValIleAsp	40
Db	286	CTAAGGCTGTCTGTAGTCAGAAATGCCTCAAAAGAGCTAGAGATGTTGTCATTGAC	345
Qy	41	IleGlnSerSerLeuSerIleGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGCAATGAGCCCGTATATATTCTCACTCAA	405
Qy	61	GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80



Db 406 GAAGCTGCATTAAATCTTGGCTTCAACAAAAACATATCAGGGACAAAGCATGTAAAC 465  
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Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACTGCTACCTATTTTCTGT 525  
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIlelle 120  
Db 526 CCCAACGAGGAGCCTGTCCATTGAAACAGCAAAAGGACTTATGAGTTACAGGATAAT 585  
Qy 121 ThrAspPheProSerLeuThrArgLeuLeuProSerGlnGluLeuProGlnGluAspSer 140  
Db 586 ACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGCCAAAGATTTACCCAGGAAGATTC 645  
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
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Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAGCCCAACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTCCCGAGCTCCTCTCTTATAAGGAA 825  
Qy 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATCTCAGAGTTCACAATTTCTCTGTATCAAGAAATAGTCATCTGTGCT 885  
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAGCCGCGCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
Qy 261 GlnProGlnLeuAlaThrAlaProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACTGTAACCACTGTCACTTCTCAGCTCCACG 1065  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTTACACGGCTGGGCTACACTCCAAGCAATGGCTACAACA 1125  
Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
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Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
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Db 1306 GAGGCCAGTCCAGGCAGTCTTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA 1365  
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheValIleGly 400  
Db 1366 TTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGTGTATAGGC 1425  
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgGlyArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTGGGTAGAAATCCTTTCCGGAATCACTCCGAGGAACGTTACTCAAGACTG 1485  
Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518  
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; Sequence 514, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C17  
; CURRENT APPLICATION NUMBER: US/09/991,163  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
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Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x US-09-991-163-514 (1-2284)

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QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60  
DB 346 ATCCAGTCATCTCTTCTAAGGGAATCAGAGGCAATGAGCCGATATATATCTCAACTCAA 405  
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
DB 406 GAAGACTGCTAATTAATCTTCTGCTTCAACAAAAACATATCAGGGGACAAAGCATGTAC 465  
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DB 466 TTGATGATCTTCGACACTCGAAACAGCTAGACAAACCAACTGCTACCTATTTTCTGT 525  
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
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QY 161 SerLysProThrAspIleSerTrpAspThrLeuSerGlnLysPheGlySerSerAsp 180  
DB 706 TCAAGCCCAACCGATATCTATGAGAGACACACTTTCTCAGAAGTTTGGATCCCTCAGAT 765  
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
DB 766 CACCTGGAGAACTATTTAAGATGGATGAAGCAGTCCCGCCAGCTCTCTTATAAGGA 825  
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
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QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
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DB 1306 GAGGCCAGTCCAGGCAGTCTTCCAGGCGAGTGTTCAGAAATAACAGTACCGCCTTCCA 1365  
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QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgTyrSerArgLeu 420  
DB 1426 CTCGCTCTCTGGGTAGAATCTTTTCGGAATCACTCCGAGGAAACGTACTCAAGACTG 1485  
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DB 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

## RESULT 14

US-09-945-015-82  
; Sequence 82, Application US/09945015  
; Patent No. US20020132768A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,015  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222  
 ; PRIOR FILING DATE: July 28, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330  
 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/216,021  
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 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020132768Aember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. US20020132768Aember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 82  
 ; LENGTH: 2284  
 ; TYPE: DNA  
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 US-09-945-015-82

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US-10-735-014-83 (1-431) x US-09-945-015-82 (1-2284)

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 Db 286 CTAAGGCTGCTGCTAGTACAGAAATGCTCAAAAGAGCTAGAGATGTTGTCATTGAC 345  
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 Db 526 CCAACGAGGAAGCTGCTCATTTGAACACGACAAAGGACTTATGAGTTACAGGATAATT 585  
 Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
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 Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspThr 160  
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 Qy 161 SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
 Db 706 TCAAAGCCCAACCGATATCTCATGGAGACACACTTCTCAGAAGTTTGGATCCTCAGAT 765  
 Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaThrLysGlu 200  
 Db 766 CACTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCAGCTCCTTGTCTTAAGGAA 825  
 Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuPro 220  
 Db 826 AAGGCCATTTCTCAGAGTTTCACTTTCTCTGTATCAAGAAATAGCTCATCTGCTGCT 885  
 Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
 Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTGTCTTCTCCACATACACCTCGGCT 945  
 Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
 Db 946 ACTCCAAAGCCCGCCCTTCTACCCACCAATGCTTCACTGACACCTTCTGGAGCTTC 1005  
 Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrValThrSerGlnProProThr 280  
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 Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
 Db 1126 GCAGTCTCTGACTACCACTTTTCAGGCACCTTACGGACTTCGAAAGGCGAGCTTAGAACCA 1185  
 Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValThrValThrAla 340  
 Db 1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245  
 Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerThrGluGlyArg 360  
 Db 1246 CTTTCTATGTCAAAATGTGGAGTCTTCCACTATCAATAAAACTGCTTCTCTGGGAAGTAGG 1305  
 Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnThrGlyLeuPro 380  
 Db 1306 GAGGCAGCTCAGGCGAGTTCCTCCAGGCGAGGTTCAGAAATCAGTACGCGCTTCCA 1365  
 Qy 381 PheGluLysThrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
 Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTATAGGC 1425  
 Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgThrSerArgLeu 420  
 Db 1426 CTCGTCTCTCTGGGTAGAATCTTTCGGGAATCACTCCGAGGAACGCTTACTCAAGACTG 1485  
 Qy 421 AspThrLeuIleAsnGlyIleThrValAspIle 431  
 Db 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 15

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; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981Aember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132981Aember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
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; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-396-82

Alignment Scores:
Pred. No.:      1,47e-211    Length:      2284
Score:          2211.00     Matches:       431
Percent Similarity:   100.00% Conservative:    0
Best Local Similarity: 100.00% Mismatches:        0
Query Match:         100.00% Indels:             0
DB:                  9           Gaps:              0

US-10-735-014-83 (1-431) x US-09-944-396-82 (1-2284)

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Db      226 ATGTTCCTCGGGAGAGAAGGAGCTTGACTTACACTTTGGTAATAATATTGCCTCCGTACA 2855
Qy      21 LeuArgLeuSerAlaSerGlnAsnCysleuLysSerLeuGluUaspValVallie Asp 40
Db      286 CTAAAGCGTGCTGCTAGTAGCAANTGCCCAAANAAGAGCTAGAGAAGATGTTGTCATTGAC 3455
Qy      41 IleginSerSerLeuSerLyegylileArgGlyAenGluProValTrThrSerrThrGln 60
Db      346 ATCCAGTCATCTCTTTCTAAGGAATCATAGGCAATGAGCCCCGTATATACTTCAACTCAA 4055
Qy      61 GluaspcyslleAasnSerCyseSerThrllysaaenllieserGlyAsplysalacysasn 80
Db      406 GAAGACATGCATTAATCTCTGCTGTTCACAAAAAACATATACAGGGGCAAGAGCATGTAAc 4655
Qy      81 LeumetillepheaspthratqlysthrAlaarGlinProAsnCsytFrrLeuphePhecys 100
Db      466 TTGATGATCTCGACACTCGAAAACACAGCTAGACAACCACCACTGCTACTCTATTTTTCTGT 5255
Qy      101 ProasnGluGluAlaCysproLeuLysprobalysglyLeumetsertyrarglilelie 120
Db      526 CCCAACGAGGAAGCCTGTGCCATTGAAACACGACAAAAGGACTTATCAGTTACAGGATAAT 5855
Qy      121 ThraspheProserLeuthrArqaasnLeuproserGlinGluLeuproGlngluaspsr 140
Db      586 ACAGATTTTCATCTTTGACCAGAAATTTGGCAAGCCAAGAGTTATCCCAGGAAGATTCT 6455
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Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
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Qy 161 SerIysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 706 TCAAAGCCACCGCATATCTCATGGAGACACACTTCTCAGAAGTTTGGATCCTCAGAT 765
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAACTATTTAAGATGATGAAGCAAGTGCCAGCTCCTTGTCTATAAGAA 825
Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
Db 826 AAAGGCCATTCTCAGAGTTCACAATTTTCTCTCATCAAGAAATAGCTCATCTCGTGCCT 885
Qy 221 GluSerValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 946 ACTCCAAAGCCGCCACCTTCTACCCCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005
Qy 261 GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr 280
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACTGTCACTTCTCAGCCTCCCAAG 1065
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Db 1066 ACCCTCATTTCTACAGTTTTCACAGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125
Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db 1126 GCAGTTCGTGACTACCACTTTCAGGCACCTACGACCTCGAAAGCAGCTTAGAACCATTA 1185
Qy 321 ProPheThrGluIleSerAsnLeuThrIleAsnThrGlyAsnValTyrAsnProThrAla 340
Db 1186 CCGTTTACAGAAATCTCCAACTTAACCTTGAACACAGGGAATGTATTAACCTTACTGCA 1245
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGAAAGGTAGG 1305
Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1306 GAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAATCAGTACGGCCTTCCA 1365
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCCTGGTGTAGGC 1425
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGlnSerLeuArgArgLysArgTyrSerArgLeu 420
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Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GATTATTGATCANTGGATCTATGTGGACATC 1518
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Search completed: April 27, 2005, 02:27:57  
Job time : 667 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 26, 2005, 22:01:01 ; Search time 3342 Seconds  
(without alignments)  
4908.947 Million cell updates/sec

Title: US-10-735-014-83

Perfect score: 2211

Sequence: 1 MFPGEGSLTYLTVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cpn2.1/USPTO.spool.p/US10735014/runat.26042005.113101.7425/app.query.fasta\_1.583  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
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Database :

EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hcc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2211	100.0	1296	9 AY401136	AY401136 Homo sapi
2	2183	98.7	1296	9 AY401137	AY401137 Pan trogl
3	1831	82.8	1965	3 CRG21081	CRG21081 full-length
	1376	62.2	853	5 BQ424639	BQ424639 AGENCOURT
c	1353	61.2	884	5 BX350141	BX350141 BX350141
6	1225	55.4	1050	1 AL525434	AL525434 AL525434
7	1176.5	53.2	1245	9 AY401138	AY401138 Mus muscu
8	1164.5	52.7	2235	3 AK033526	AK033526 Mus muscu
9	1164.5	52.7	2265	3 AK018635	AK018635 Mus muscu

10	1164.5	52.7	2265	3	AK046837	Mus muscu
11	1164.5	52.7	2286	3	AK018660	Mus muscu
12	1164.5	52.7	2375	3	AK033557	Mus muscu
13	1079	48.8	623	7	CV024215	1439 Full
14	1063	48.1	753	7	CF595929	AGENCOURT
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17	1019	46.1	940	2	BF683169	602139129
18	1008	45.6	582	5	BP375799	BP375799
19	1000	45.2	697	5	BUI72626	AGENCOURT
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21	985	44.5	584	5	EX485439	DFPZP686C
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23	862.5	39.0	1036	1	AL549886	AL549886
24	852	38.5	699	4	BG720669	60292553
25	807	36.5	870	2	BF312571	601897547
26	790	35.7	697	7	CN365249	170005999
27	780.5	35.3	805	1	AU138119	AU138119
28	767	34.7	668	7	CR834065	4058249 B
29	765	34.6	447	5	BP246319	BP246319
30	764.5	34.6	855	1	AU123305	AU123305
31	755	34.1	602	5	BU789700	1044009.X
32	743.5	33.6	718	7	CK971151	4087056 B
33	709	32.1	687	5	EX953184	DRFZP781N
34	683	30.9	441	4	BI031052	IL5-MT026
35	679	30.7	457	2	AW752992	QVO-CT022
36	671	30.3	734	7	CO879641	BovGen. 07
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#### ALIGNMENTS

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DEFINITION	AY401136	genomic survey sequence.			
VERSION	AY401136.1	GI:39757125			
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SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1296)	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1296)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..1296				



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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1. >1296
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gene
ORIGIN
Alignment Scores:
Pred. No.: 2,748-191 Length: 1296
Score: 2211.00 Matches: 431
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x AY401136 (1-1296)

Qy 1 MetPheGlyGlyGluGlySerLeuThrTyrThrLeuValIleLeuCysPheLeuThr 20
Db 1 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTTGACA 60
Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
Db 61 CTAGGCTGTCTGCTAGTACAGAAATTCCTCAAAAAGAGCTAGAGAAGATGTTGTCATTGAC 120
Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyGlnGluProValTyrThrSerThrCln 60
Db 121 ATCCAGTCATCTCTTTCATAGGAATCAGAGCAATGAGCCCGTATATATCTTCAACTCAA 180
Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 181 GAAGACTGCATTAATCTTCTGTTTCAACAAAACATATCAGGGCAAGAGATGTAAC 240
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
Db 241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCAACTGCTACTATTTTCTGT 300
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
Db 301 CCCAACAGAGAGAGCTGTCATTTGAACCAAGAAAGAGCTATGAGTTACAGGATTAAT 360
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Db 481 TCNAAGCCCAACGATATCTCATGAGAGACACACTTCTCAGAAGTTGGATCTCATGAT 540
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Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
Db 661 GAAATGTGAGTGGCTCCAGCTACGGTGCGAGTTGCTTCTCCACATACCACTCCGCT 720
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 721 ACTCCAAAGCCGCCACCCCTTCTACCCCAACCAATGCTTCAGTGACACCTTCTGGGACTTCC 780
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
Db 781 CAGCCACAGCTGGCCACCACAGCTCCACTGTAAACCACTGTCACTTCTCAGCTCCGCCACG 840

RESULT 2
AY401137 1296 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY401137
VERSION AY401137.1 GI:39757126
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; PAN.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1296)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1..1296
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1. >1296
/locus_tag="HCM0790"

gene
ORIGIN
Alignment Scores:

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Pred. No.: 9,96e-189 Length: 1296
Score: 2183.00 Matches: 426
Percent Similarity: 98.84% Conservative: 0
Best Local Similarity: 98.84% Mismatches: 5
Query Match: 98.73% Indels: 0
DB: 9 Gaps: 0

US-10-735-014-83 (1-431) x AY401137 (1-1296)

QY 1 MetPhePheGlyGlyGlySerLeuThrThrLeuValIleIleCysPheLeuThr 20
DB 1 ATGTTCTTTGGGGAGAGGAGCTTACTTATACCTTTGGTAATATTTGCTTCTCGACA 60
QY 21 LeuArgLeuSerAlaSerGlnGlnCysLeuLysSerLeuLeuValIleLeuAsp 40
DB 61 CTAAGGCTGCTGCTAGTACAGAAATGCTCAACAGAGCTAGAGAGATGTTGTCATTGAC 120
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrSerThrGln 60
DB 121 ATCCAGTCACTCTTTCTTAAGGAATCAGAGGCAATGAGCCGCTATATATCTCAACTCAA 180
QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
DB 181 GAAGACTGCATTAATTTCTTGCTTCAACAAAACATATCAGGGACAAAGCATGTATAC 240
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
DB 241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCACTGCTTACCTCTTTTCTGT 300
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
DB 301 CCCAATGAGGAGCCCTGCTCCATGAAACCAAGCAAGGACTTATGAGTTACAGGATAAT 360
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
DB 361 ACAGATTTCCATCTTTGACGAGAAATTTGCCAGCAGAGATTACCCAGGAGAGATTTCT 420
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
DB 421 CTCCTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 480
QY 161 SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
DB 481 CAAAGCCCAACCGCATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCCTCAGAT 540
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
DB 541 CACTTGGAGAACTATTTAAGATGGATGAAGCAAGTCCAGCTCTTCTGTTATAGGNA 600
QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
DB 601 AAAGGCCATTTCTCAGAGTTTCAAGATTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 660
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
DB 661 GAAATATGTAGTCGCTCCAGCTACGGTGGAGATGCTTCTCCACATACCACTCCGCT 720
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
DB 721 ACTCCAAAGCCCAACCACTTTCTACCCCAATGCTTCTAGTGACACCTTCTGGGACTTCC 780
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
DB 781 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCTCTCAGCCTCCAGC 840
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
DB 841 ACCCTCATTTCTACAGTTTTTACAGGGCTGGGGCTACACTCCAAGCAATGGCTACAACA 900
QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
DB 901 GCAGTTCTGACTACCACTTTTTCAGGCACCTTACGGACTCGAAAGGCGGCACTAGAAACCAT 960

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QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
DB 961 CCGTTTACAGAAATCTCCAACCTAACTTTTGAACACAGGGAATGTGTATAACCTTACTGCA 1020
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360
DB 1021 CTTTCTATGTCAATGTGGAGTCTTCCACTAGCAATAAACTGCTTCTCTGGGNAAGTAGG 1080
QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
DB 1081 GAGGCCAGTCCAGGAGTTCGTCGCCAGGCGAGTGTTCAGAGAAATCAGTACGCGCTTCCA 1140
QY 381 PheGluLysTyrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
DB 1141 TTTGAAAATGGCTCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGGTATAGGC 1200
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420
DB 1201 CTCGTCTCTCTGGGTAGATCTCTTGGATCACTCCGCGAGGAACTTACTCTAGACTG 1260
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
DB 1261 GATTATTGATCAATGGGATCTATGTGGACATC 1293

RESULT 3
CR621081 1965 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1054YH07 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR621081
VERSION CR621081.1 GI:50501888
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1965)
AUTHORS Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1965
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YH07"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores: 3,05e-156 Length: 1965
Pred. No.: 1831.00 Matches: 357
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 82.81% Gaps: 0
DB: 3

US-10-735-014-83 (1-431) x CR621081 (1-1965)

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QY 75 GlyAspLysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgLysProAsn 94  
 Db 147 GGGGCAAGCATGTAACTTGATGATCTGCACACTCGAAAAACAGCTAGACACCCCAAC 206  
 QY 95 CysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu 114  
 Db 207 TGCTACCTATTTTCTGCTCCACAGGAGGCTGCTCCATTGAACACCAAGAGGACTT 266  
 QY 115 MetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGlu 134  
 Db 267 ATGAGTTACAGGATAATACAGATTTTCATCTTTGACACAGAAATTTGCCAAGCAACAG 326  
 QY 135 LeuProGlnGluAspSerLeuLeuHISGlyGlnPheSerGlnAlaValThrProLeuAla 154  
 Db 327 TTACCCAGGAGATCTCTCTTACATGGCCAAATTTTTCACAGCAGTCACTCCCTTAGCC 386  
 QY 155 HisHisThrAspTyrSerLysProThrAspIleSerTyrArgAspThrLeuSerGln 174  
 Db 387 CATCATCACACAGATTTATCAAGGCCACCGATATCTCATGGAGAGACACACTTCTCAG 446  
 QY 175 LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194  
 Db 447 AAGTTTGGATCTCTAGATCACTTGGAGAACTATTAAAGATGGATGAAGCAAGTCCCCAG 506  
 QY 195 LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214  
 Db 507 CTCCTTGCTTATAGGAAAGGCCATCTCTAGAGTTCAATTTTCTCTGATCAGAA 566  
 QY 215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234  
 Db 567 ATAGCTCATCTGCTGCTGAAATGTGAGTGGCTGCCCTCCAGCTACGGTGGCAGTTGCTCT 626  
 QY 235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254  
 Db 627 CCACATACCACTCGGCTACTCCAAAGCCGCCACCTTCTACCCACCAATGCTCTAGTG 686  
 QY 255 ThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThrVal 274  
 Db 687 ACACCTTCTGGAGCTTCCAGCCACAGCTGGCCACCAAGCTCCACCTGTAACCACTGTC 746  
 QY 275 ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294  
 Db 747 ACTTCTCAGCTCCACACCACTCATTTCTACAGTTTTTACACGGCTGCGGTACACTC 806  
 QY 295 GlnAlaMetAlaThrThrAlaValLeuThrThrPheGlnAlaProThrAspSerLys 314  
 Db 807 CAAGCAATGGGTACAAACAGCAGTCTGACTACCACTTTCAGGCACTTACGGACTCGAAA 866  
 QY 315 GlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsn 334  
 Db 867 GGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCAACCTTAATTTGAACACAGGGAAT 926  
 QY 335 ValTyrAsnProThrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThr 354  
 Db 927 GTGTATAACCTTACTGCACTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACT 986  
 QY 355 AlaSerTyrGlyArgGluAlaSerProGlySerSerSerGlnGlySerValProGlu 374  
 Db 987 GCTTCTCGGAGGTAGGGAGGCCAGTCCAGGAGTTCCTCCCGGGCAGTGTTCACGAA 1046  
 QY 375 AsnGlnTyrGlyLeuProPheGluLysThrLeuLeuIleGlySerLeuLeuPheGlyVal 394  
 Db 1047 AATCAGTACGGCTTCCATTTGAAATGGCTTCTTATCGGTCCTCTCTTTGGTGTG 1106  
 QY 395 LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArg 414  
 Db 1107 CTGTTCTCTGGGTAGGGCTCGTCTCTCTGGGTAGAATCTCTCGGAATCACTCCGCGAG 1166  
 QY 415 LysArgTyrSerArgLeuAspTyrLeuIleAsnGlyIleTyrValAspIle 431  
 Db 1167 AAACGTTACTCAAGACTGGATTTATTTGATCAATGGATCTAATGGATC 1217

## RESULT 4

BQ424639

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ424639  
 AGENCOURT 7896936 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6159709  
 5', mRNA sequence.  
 BQ424639  
 BQ424639.1 GI:211119954  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 853)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-x@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DMP  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM13509 row: d column: 14  
 High quality sequence stop: 735.  
 Location/Qualifiers  
 1..853  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6159709"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 72"  
 /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."

## FEATURES

source

Alignment Scores:  
 Pred. No.: 3,37e-115 Length: 853  
 Score: 1376.00 Matches: 272  
 Percent Similarity: 99.28% Conservatives: 2  
 Best Local Similarity: 98.55% Mismatches: 0  
 Query Match: 62.23% Indels: 2  
 DB: 5 Gaps: 0

US-10-735-014-83 (1-431) x BQ424639 (1-853)

QY 73 IleSerGlyAspLysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGln 92

Db 17 ATTGCAAGGGACAAAGCATGTAATCTGATGATCTTCACACTCGAAAAACAGCTAGACAA 76

QY 93 ProAsnCysTyrLeuPhePheCysProAsnGluAlaCysProLeuLysProAlaLys 112

Db 77 CCCAACTGCTTACCTATTTTCTGTCACAGGAGGCTGCTCATTTGAACACGACAAA 136

QY 113 GlyLeuMetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSer 132

Db 137 GGACTTATGAGTTACAGGATAATACAGATTTTCCATCTTTGACCAAGAAATTTGCCAAGC 196

QY 133 GlnGluLeuProGlnGluAspSerLeuLeuHISGlyGlnPheSerGlnAlaValThrPro 152

Db 197 CAAGAGTATCCCGAGGAGATCTCTTCTTACATGGCCAAATTTTCAAGCAGTCACTCC 256

QY 153 LeuAlaHisHisThrAspTyrSerLysProThrAspIleSerTyrArgAspThrLeu 172

Db 257 CTAGCCCATCATCACAGATTTATTAAGCCCAACCGATATCTCATGGAGAGACACTT 316

QY 173 SerGlnLysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSer 192

```

Db      317 TCTCAGAGTTGGATCCTCAGATCACCTGGGAAACTATTAAAGATGATGAAGCAAGT 376
Qy      193 AlaGlnLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAsp 212
Db      377 GCCCAGCTCTTGCTTATTAAGGAAGGCAATCTCAGAGTTCAAAATTTTCCTCTGAT 436
Qy      213 GlnGluLeuAlaHisLeuLeuProGluAenValSerAlaLeuProAlaThrValAlaVal 232
Db      437 CAAGAAATAGCTCATCTGCTGCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTT 496
Qy      233 AlaSerProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAla 252
Db      497 GCTTCTCCACATACCACTCGGCTACTCCAAAGCCCGCCACCTTCTACCCCAATGCT 556
Qy      253 SerValThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr 272
Db      557 TCAGTGACACCTCTGGGACTTCCAGCCACAGCTGGCCACACAGCTCCACCTGTAAAC 616
Qy      273 ThrValThrSerGlnProProThrThrLeuLeuSerThrValPheThrArgAlaAla 292
Db      617 ACTGTCACTTCTCAGCTCCACGACCTCAATTTCTACAGTTTTCACGGGCTGGGCT 676
Qy      293 ThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrPheGlnAlaProThrAsp 312
Db      677 ACATCCCAAGCAATGGCTACAAAGAGTCTGACTTACCACCTTTTACGGCAGCTACGGAC 736
Qy      313 SerLysGlySerLeuGluThrThrProPheThrGluLeuSerAsnLeuThrLeuAlaThr 332
Db      737 TCGAAGGAGGAGCTTAGAACCAATACGTTTACAGAAATCTCCACTTAATTTGAACACA 796
Qy      333 GlyAenValTyrAsn-ProThrAlaLeuSerMetSerAsnVal 346
Db      797 GGGGAATGTGTATAACCCCTACTGCACCTTCTATGTCAATGTG 840

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## RESULT 5

```

BX350141/c
LOCUS      BX350141 Homo sapiens 884 bp mRNA linear EST 08-APR-2004
DEFINITION clone CS0D1054YH07 3-PRIME, mRNA sequence.
ACCESSION  BX350141
VERSION     BX350141.1
KEYWORDS    GT:30365418
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6656.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAI0232A03_CS02129_1&c=6656.r

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## FEATURES

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source
Location/Qualifiers
1..884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YH07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo(dT)

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primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

```

ORIGIN
Alignment Scores:
Pred. No.: 4,53e-113 Length: 884
Score: 1353.00 Matches: 283
Percent Similarity: 97.26% Conservatives: 1
Best Local Similarity: 96.92% Mismatches: 8
Query Match: 61.13% Indels: 3
DB: 5 Gaps: 0
US-10-735-014-83 (1-431) x BX350141 (1-884)
Qy 125 SerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeuLeuHisGly 144
Db 882 TCTTGGACCAAGAAATTTGGCAAGCCACAGAGTTACCAG-GAAGATTTCTCTTACATGGC 824
Qy 145 GlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyrSerLysProThr 164
Db 823 AA-TTTTCAAGCAGTCACTCCCTAGCCATCATCACAGATTTATTTCANAGCCACC 765
Qy 165 AspLeuSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLys 184
Db 764 AATATCTCATGGAGACACACT-TCTCAGAAAGTTTGTATCCCTCAGATCACCTGGAGAA 706
Qy 185 LeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSer 204
Db 705 CTATTTAGATGGATGAAGCAAGTCCAGCTCTTGTCTTATAGGAAAGGCCAATCT 646
Qy 205 GlnSerSerGlnPheSerSerAspGlnGluLeuAlaHisLeuLeuProGluAenValSer 224
Db 645 CAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCTGAAAATGTGAGT 586
Qy 225 AlaLeuProAlaThrValAlaValAlaSerProHisHisThrThrSerAlaThrProLysPro 244
Db 585 GCGCTCCAGCTTCCACCTGTAACTTCTTCCACATACCACCTCGGTACTCTCCAAAGCCC 526
Qy 245 AlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnProGlnLeu 264
Db 525 GCCACCTTCTACCCACCAATCTTCAGTGACACCTTCTGGGACTTCCCGCCACAGCTG 466
Qy 265 AlaThrThrAlaProProValThrThrValThrSerGlnProProThrThrLeuLeuSer 284
Db 465 GCCACCAAGCTTCCACCTGTAACTTCTTCTGAGCTTCCAGCTTCCAGACCTCATTTCT 406
Qy 285 ThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThrAlaValLeuThr 304
Db 405 ACAGTTTTTACACGGGCTCGGCTACACTCCAAAGCAATGGCTTACAACAGCAGTCTTGACT 346
Qy 305 ThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIleProPheThrGlu 324
Db 345 ACCACCTTTCAGGACCTTACGAGCTTCAAAAGGAGCTTAGAAACCATACCGTTACAGAA 286
Qy 325 IleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeuSerMetSer 344
Db 285 ATCTCCAATTAACCTTGAACACAGGGAATGTGTATTAACCTTACTGCACTTTCTATGTCA 226
Qy 345 AenValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArgGluAlaSerPro 364
Db 225 AATGGAGTCTTCCACTATGAATAAACTGCTTCTCGGAGAGGTAGGAGGCCAGTCCA 166
Qy 365 GlySerSerGlnGlySerValProGluAenGlnTyrGlyLeuProPheGluLysTyr 384
Db 165 GGCAGTCTCTCCAGGCGAGTGTTCAGAAATATAGTAGCGGCTTCCATTTGAAAATGG 106
Qy 385 LeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGlyLeuValLeuLeu 404
Db 105 CTTCTTATCGGGTCCCTGCTCTTGTGTCCTGTTCTTCTGGTATAGGCTCTGCTCTCTG 46
Qy 405 GlyArgIleLeuSerGluSerLeuArgLysArg 416

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Db      45  GGTAGATCTCTCGGAATCACTCGCAGGAAACGT 10

RESULT 6
AL525434      1050 bp      mRNA      linear      EST 24-MAR-2004
LOCUS      AL525434 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION  CDNA clone CS0DC011YG07 5-PRIME, mRNA sequence.
ACCESSION   AL525434
VERSION     AL525434.3 GI:45700628
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1050)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:31063298.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Crenieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6656.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?c=CS0DC011AD04QPl&c=6656.r.

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            /note="1st strand cDNA was primed with a NotI-oligo(dT)
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ORIGIN
Alignment Scores:
Pred. No.:      3.05e-101      Length:      1050
Score:          1225.00      Matches:      244
Percent Similarity: 93.13%      Conservative: 0
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US-10-735-014-83 (1-431) x AL525434 (1-1050)

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Qy      21  LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40
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Qy      41  IleGlnSerSerLeuSerLysGlyLleArgGlyAsnGluProValTyrrThrSerThrGln 60
Db      368  ATCCAGTCATCTCTTTCTAAGGAATCAGAGCGAATGAGCCCGTATATCTTCAACTCAA 427

Qy      61  GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db      428  GAAGACTGCATTAATTCCTGTTTCAACAAAAACATATCAGGGGCAAAAGCATGTAC 487

Qy      81  LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrrLeuPheCys 100

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Db      488  TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCCACTACCTATTTTCTGT 547

Qy      101  ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrrArgIleIle 120
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Qy      121  ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
Db      608  ACAGATTTTCAATCTTTGACCAAGAAATTTGCCAAGCCCAAGAGTTACCCAGGAGATCTCT 667

Qy      141  LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
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Qy      161  SerLysProThrAspTlleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db      728  TCAAAAGCCCAACCATATCTCATGGAGAGACACACTTTTCTCAGAAGTTTGGATCTCAGAT 787

Qy      181  HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrrLysGlu 200
Db      788  CACTCGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCGAGCTCTGCTTATTAAGAA 847

Qy      201  LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluLeuAlaHisLeu-LeuPr 220
Db      848  AAAAGGCCATCTCAGAGTTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCCTGCC 907

Qy      220  oGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAl 240
Db      908  TGAATAATGTAGTGCGCTCCAGCTACGTGGGAGTTGCTTCTCCACATACMACTC--GG 965

Qy      240  aThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSe 260
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Qy      260  rGln 261
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LOCUS      Mus musculus HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION  genomic survey sequence.
ACCESSION   AY401138
VERSION     AY401138.1 GI:39757127
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
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            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
            Science 302 (5652), 1960-1963 (2003)
            14671302
            2  (bases 1 to 1245)
            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
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Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
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Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1210 GACTACTTGATCAACGGGATCTATGTTGATC 1242

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DEFINITION  
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AK033526  
AK033526.1 GI:26329204  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
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REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PubMed 10349636  
REFERENCE  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20493374  
PubMed 11042159  
REFERENCE  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tadhiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujimoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yamawake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PubMed 11076861  
REFERENCE  
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9216, Fax: 81-45-503-9216)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Location/Qualifiers

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US-10-735-014-83 (1-431) x AK033526 (1-2235)

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REFERENCE
AUTHORS
6 (bases 1 to 2265)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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Alignment Scores:
Pred. No.: 3,54e-95 Length: 2265
Score: 1164.50 Matches: 258
Percent Similarity: 68.45% Conservative: 37
Best Local Similarity: 59.86% Mismatches: 119
Query Match: 52.67% Indels: 17
DB: 3 Gaps: 6
US-10-735-014-83 (1-431) x AK045837 (1-2265)
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.

# TITLE JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>.

## FEATURES

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Percent Similarity:	68.45%	Conservative:	37
Best Local Similarity:	59.86%	Mismatches:	119
Query Match:	52.67%	Indels:	17
DB:	3	Gaps:	6

US-10-735-014-83 (1-431) x AK033557 (1-2375)

Qy	1	MetPheGlyGlyGluGlySerLeuThrThrLeuValIleCysPheLeuThr	20
Db	372	ATGCTCTTCAGGGAAC--AGCTGGCTACTGTGTGGTCATTCCTCTCGACA	428
Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp	40
Db	429	CCAGGTCGTCGTGCTGAGAACTGCTCACCAGAGCTAGAGAGCTGTGTCATGAC	498
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValThrThrGln	60

Db	489	ATCCAAATCGTCGCTTTCAAAAGGCAATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG	548
Qy	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	549	GAAAGACTGATCGTGCTCTCTTCAACAAAAGACATAGCAGGGGACAGGATGTAAT	608
Qy	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysValLeuPhePheCys	100
Db	609	TTGATGATCTTTGACCCCGAAGACAGACAGACAGCCCACTGCTACCTGTGTTCTGT	668
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerThrArgIleIle	120
Db	669	CCCAGCGAGGATGCTGTCGCTGAAAGCCAGCCAGGCGCTTGTGACCTACAGGCTCATC	728
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
Db	729	AGAGATTTTCGCTGACCGAGCGCTAATTCATCACTCCAAACAGTTAACACAGAGAGATT	788
Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160
Db	789	CTCTTACTTGCACCATTCGTCACAGGAGCCACCCCTGGGTTTCGTACCCAGCAGGTAC	848
Qy	161	SerLysProThrAspIleSerThrArgAspThrLeuSerGlnLysPheGlySerSerAsp	180
Db	849	CCAAAGCCACCGCGCTGCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCTG	908
Qy	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200
Db	909	CACCTTCGCAACACATCAAGGCTGATGAACAAAGCATCGAGCTC-----CCTGAAGAA	962
Qy	201	LysGlyHisSerGlnPheSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
Db	963	AAAAGCCATCTCAGAGTTTACAGCTTCCCTCAGAATAAATAGTGTATCTGCTCCCT	1022
Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
Db	1023	AAAAATGTGCGGACTCCACCTACCACTGAGCTGTGGCTCCCTCCGTAACGCTCTCGCC	1082
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	1083	ACCTTGAAGCCTGAGCTTCTGTGTTG---ACCAGCATTTCTAGTCAGACTAAGACTTTGAAG	1139
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrValThrSerGlnProProThr	280
Db	1140	CAGAAAGGAG---GCCACCACAGCATCACCTGTGCACCCGTCGACCTCGAAGCTCCAGGA	1196
Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1197	GTCCCAAGGCTTACAAAGTTTACA-----CCCCGTGGTTACACATCAG	1238
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1239	GCAGCTTTGACTAACACCTTTTACGACATACATACAGACTCCAAAGGCGATCTTAGAAACA	1298
Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1299	CCCTTTCAGGAGGCTCTACGCTGACT-----TCAGACCCGAGGCAC	1340
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1341	GGGAAAAGCTCAACCTCAGAGTCTTCCATTCAAAACACAGACTGCTTCTCTGGGAGGACAG	1400
Qy	361	GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1401	AGGCTCAGTGTAGGAGCGCATCGCTGAACAGGGGTCCAAAAGCCAGCATGCGCTTTCA	1460
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1461	TTTGAGAGTGGCTCTCATTTGGGACCCCTCTTGTGGTGTGTTTGTCTGGTAAATAGGT	1520
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu	420
Db	1521	CTCGTCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGCTATTCAAGACTT	1580

QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
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 Db 1581 GACTACTTGATCAACGGGATCTATGTTGACATC 1613

RESULT 13  
 CV024215  
 LOCUS  
 DEFINITION  
 1439 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC032998, mRNA sequence.

ACCESSION  
 CV024215  
 VERSION  
 CV024215.1 GI:51482047  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 623)  
 Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Cusick,M.E., Albaia,J.S., Hill,D.E. and Vidal,M. Human ORFome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidal@dfci.harvard.edu  
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers  
 FORWARD: ATGTCTTCGGGGAGAGGGAG  
 BACKWARD: TAGATGTCACATAGATCCCAT  
 Insert Length: 623 Std Error: 122.00  
 Plate: 11036 row: 12 column: E  
 Seq primer: ACTGGCCGTCGTTTACACAGTCGTCGACTGGGAAAC  
 High quality sequence start: 94  
 High quality sequence stop: 622  
 POLYA=No.

FEATURES  
 source  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="mixed"  
 /clone\_lib="Full Length cDNA from the Mammalian Gene Collection"  
 /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,01e-88 Length: 623  
 Score: 1079.00 Matches: 204  
 Percent Similarity: 99.03% Conservatives: 1  
 Best Local Similarity: 98.55% Mismatches: 2  
 Query Match: 48.80% Indels: 0  
 DB: 7 Gaps: 0

US-10-735-014-83 (1-431) x CV024215 (1-623)

QY 1 MetPheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr 20  
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Db 1 ATGTTCTTCGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 60  
 QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40  
 |||||  
 Db 61 CTAAGGCTGTCTGCTAGTCAGAAATTCCTCAAAAAGAGCTCTAGAGATGTTGTCATTGAC 120  
 QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
 |||||  
 Db 121 ATCCAGTCATCTCTTCTTAAGGGAATCAGAGCAATGAGCCCATATATATCTCAACTCAA 180  
 QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
 |||||  
 Db 181 GAAGACTGCATTAATTTCTTGTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 240  
 QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
 |||||  
 Db 241 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCCAACTGTACTATTTTCTGT 300  
 QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
 |||||  
 Db 301 CCCAACGAGGAAGCCTGTCATTGAACCCAGCAAAAGGACTTATGAGTTACAGGATAATT 360  
 QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
 |||||  
 Db 361 ACAGATTTTCCATCTTTGACCATTAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTCT 420  
 QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
 |||||  
 Db 421 CTCATTACATGGCCAAATTTTCACAGAGTCATCTCCCTAGCCCATCATCACAGATTAT 480  
 QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
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 Db 481 TCAAGAACCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCTCAGAT 540  
 QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
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 Db 541 CACTTGGAGAAACTATTTAAGATGGATGAAGCATGTGCCACGCTCTTCTTATATAGGAA 600  
 QY 201 LysGlyHisSerGlnSerSer 207  
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 Db 601 AAAGGGCATTTCTCAGAGTTCA 621

RESULT 14  
 CF595929  
 LOCUS  
 DEFINITION  
 AGENCOURT 15668985 NCI CGAP\_Sc3 Homo sapiens cDNA clone  
 IMAGE:30703562 5', mRNA sequence.

ACCESSION  
 CF595929  
 VERSION  
 CF595929.1 GI:36351906  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 753)  
 NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS  
 National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE  
 JOURNAL  
 COMMENT  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Arnold Schwartz, MD, PhD  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDCM251 row: d column: 03  
 High quality sequence stop: 540.  
 Location/Qualifiers

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/clone="IMAGE:30703562"
/tissue_type="Stomach, adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP St3"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgcttcgccc); Library is oligo-dT primed
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.30
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

ORIGIN

Alignment Scores:	1.18e-86	Length:	753
Pred. No.:	1063.00	Matches:	219
Score:	97.77%	Conservative:	0
Best Local Similarity:	97.77%	Mismatches:	3
Query Match:	48.08%	Indels:	2
DB:	7	Gaps:	0

US-10-735-014-83 (1-431) x CF595929 (1-753)

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QY 175 LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194
DB 5 AAGTTTGATCTCTCAGATCACTTGGAGAACTATTAAAGATGGATGAAGCAAGTCCCGAG 64

QY 195 LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerAspGlnGlu 214
DB 65 CTCCTTGCTTATAAGGAAAGAGGCAATCTCTCAGAGTTTCAACAATTTCTCTGTGATCAAGAA 124

QY 215 IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
DB 125 ATAGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184

QY 235 ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254
DB 185 CCACATACCACTCGCTACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTG 244

QY 255 ThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrVal 274
DB 245 ACAGCTTCTGGGACTTCCAGCCAGCTGCGCCACCAAGCTCCACCTGTAACCACTGTC 304

QY 275 ThrSerGlnProThrThrLeuLeuSerThrValPheThrArgAlaAlaAlaThrLeu 294
DB 305 ACTTCTAGCTCCACAGCCCTCATTTCTACAGTTTACAGGGCTGGGGCTACACTC 364

QY 295 GlnAlaMetAlaThrAlaValLeuThrThrPheGlnAlaProThrAspSerLys 314
DB 365 CAAGCAATGGCTACACAGCAGTCTGACTACCACTTTTCAGGCACTACGAGTCCGAA 424

QY 315 GlySerLeuGluThrIleProPheThrGluLeuSerAsnLeuThrLeuAsnThrGlyAsn 334
DB 425 GGCAGCTTTAGAAACCATACCTTTTACAGAAATCTCCAACTTAATTTTGAACACAGGGAAT 484

QY 335 ValTyrAsnProThrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThr 354
DB 485 GTGTATATACCTACTGACTTTCTATGTCAAATGTGAGTCTCCATCATGATTAATAACT 544

QY 355 AlaSerTrpGluGlyArgGluAlaSerProGlySerSerGlnGlySerValProGlu 374
DB 545 GCTTCTCTGNGAAGGTAGGAGGCGGAGTCCAGGCAAGTTTCTCCAGGGCAGTGTTCACAGAA 604

QY 375 AsnGlnTyrGlyLeuProPheGluLysTrpLeuLeuLeuGlySerLeu-LeuPhe-GlyV 394
DB 604
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105 AATCAGTACCGCTTCCATTTGAAATGCTTCTTATCGGCTCCCTGCTTGGTG 664

394 alleuPhe 396

665 TCCTGTTC 672

RESULT 15

AK002644

LOCUS

DEFINITION

Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610017A09 product:weakly similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert sequence.

ACCESSION

AK002644

VERSION

AK002644.1 GI:12832780

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2227)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Koike, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Taya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome



Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
Please visit our web site (http://genome.gsc.riken.jp/) for further details.

## COMMENT

cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cdna was primed with a primer .15' GAGAGAGACGGCCGACCTGAGTTTCTTTTCTTTTNN 3', cdna was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cdna went through one round of normalization to Rot = 5.0. Second strand cdna was prepared with the primer adapter of sequence [5' GAGAGAGAGAGGATCCAGAGCTCAATTAATTAATTAACCCGCCCC 3']. cdna was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

## FEATURES

## Location/Qualifiers

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/clone="0610017A09"
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/issue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cdna library"
/dev_stage="adult"
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## ORIGIN

## Alignment Scores:

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Pred. No.: 2,9e-85 Length: 2227
Score: 1056.00 Matches: 248
Percent Similarity: 66.36% Conservative: 38
Best Local Similarity: 57.54% Mismatches: 128
Query Match: 47.76% Indels: 20
DB: 3 Gaps: 6

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US-10-735-014-83 (1-431) x AK002644 (1-2227)

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QY 21 LeuArgLeuSerAlaSerGlnAnCysLeuLysSerLeuGluAspValIleLeu 40
Db 337 CCAAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrGln 60
Db 397 ATCCATCTGCTGCTTCAAAAGGCATTCAGGCAATGAGCCCATACACTTGGCACTCAG 456
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 457 GAAGACTGTATCGGTGCTGCTGCTTCAAAAAGACATAGCAGGGGACAGGCATGTAAT 516
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
Db 517 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTGCTGCTGCTGCT 576
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
Db 577 CCGAGGAGGATGCTCTGCTGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 636
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

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Search completed: April 27, 2005, 00:58:02  
Job time : 3367 secs

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QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
Db 697 CTCTTACTTGACCATTCGTCCAGGAGCCACCCCTGGGTTTCGTATCCACGAGGAGTTAC 756
QY 161 SerLysProThrAspLysSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 757 CCAAAGCCACCCGCTGCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCTG 816
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 817 CACTTGCAGCAACACATCAAGGCTGATGAACAAGCATGCAGCTC-----CCTGAAGAA 870
QY 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluLeuLeuAlaHisLeuLeuPro 220
Db 871 AAAAGCCATCTCAGAGTTTACAGCTTCCCTCAGAACTAAATAATGGCTCATCTGCTCCCT 930
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
Db 931 AAAACTGTGCGGACTCCACCTACCACTGTAGCTGTGGCTCCCTCCGTAACGCTCTCTGCC 990
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 991 ACCCTGAAGCCTGAGCTTCTGTTG---ACCAGCATTTTCACTGACAGCTAAGACTTTGAAG 1047
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
Db 1048 CAGAAGGAG--GCCACACACATCCTGTGACACCGTACCTGCAAGCTCCAGGAGTCCAGGA 1104
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Db 1105 GTCCCGGGTCTTACAAGTTTTTACA-----CCCGTGGTTACACATCAG 1146
QY 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
Db 1147 GCAGCTTTGACTTAACACCTTTTCAGGCACATACAGACTCCAAAGGCACTCTTAGAAACAATG 1206
QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
Db 1207 CTTTTTCAAGGAGGCTCTACGCTGACT-----TCAGACCCGAGGCAC 1248
QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360
Db 1249 GGGAAAAGCTCAACCTCAGAGCTTCCATTACAAACAGAGCTGCTTCTGGGAGGACAGG 1308
QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
Db 1309 AGGGTCAGTGTAGGCGGCGCATCGCTGAACAAGGGTCCAAAAGGCGAGCATGT-CTTACA 1367
QY 381 PheGluLysTyrLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
Db 1368 TTTGAGAAGGG-TCTCTCATCGGACCCATCTCTGG-TGTGTTATTTGTTGGTAAGTAGCT 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgTyrSerArgLeu 420
Db 1426 CTCGCTCTCTTGGGTAGGATGCTGTTGAAGCCCTCCGTTAGGAAACGGTATTTCAGACTT 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GACTACTTGATCAACGGGATCTATGTTGACATC 1518

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